

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Human G P				
OM protein - protein search, using sw model	PSNRSSLESENATSLTTF 372	ADC22539 Human CXC				
Run on: August 29, 2005, 23:43:51 ; Search time 166 Seconds (without alignments)	866.716 Million cell updates/sec	Adf17988 Human GPR				
Title: US-10-666-689-6	866.716 Million cell updates/sec	Adh14012 Human GPR				
Perfect score: 1953	866.716 Million cell updates/sec	Adn39434 Cancer/an				
Sequence: 1 MNPLTLEMLENEDLFWE.....PSNRSSLESENATSLTTF 372	866.716 Million cell updates/sec	Adh61810 Human G P				
Scoring table: BLOSUM62	866.716 Million cell updates/sec	Ado29458 Human GPC				
Gapop 10.0 , Gapext 0.5	866.716 Million cell updates/sec	Adp12496 Protein e				
Searched: 2105692 seqs, 386760381 residues	866.716 Million cell updates/sec	Adp12922 Protein e				
Total number of hits satisfying chosen parameters: 2105692	866.716 Million cell updates/sec	Adq09119 Human CXC				
Minimum DB seq length: 0	866.716 Million cell updates/sec	Adq95936 T cell ac				
Maximum DB seq length: 2000000000	866.716 Million cell updates/sec	Adr67008 Human can				
Post-processing: Minimum Match 0% Maximum Match 100%	866.716 Million cell updates/sec	Adr73812 Human CXC				
Database : A_Geneseq_16Dec04:*	866.716 Million cell updates/sec	Aay50129 Human che				
1: geneseqP1980b:*	866.716 Million cell updates/sec	Adc46963 Human CXC				
2: geneseqP1990b:*	866.716 Million cell updates/sec	Adh61808 Human G P				
3: geneseqP2000b:*	866.716 Million cell updates/sec	Adq95988 T cell ac				
4: geneseqP2001b:*	866.716 Million cell updates/sec	Aay90648 Human mut				
5: geneseqP2002b:*	866.716 Million cell updates/sec	Adc22693 Human G P				
6: geneseqP2003b:*	866.716 Million cell updates/sec	Adh14166 Mutated h				
7: geneseqP2004b:*	866.716 Million cell updates/sec	Adq73816 Human non				
8: geneseqP2005b:*	866.716 Million cell updates/sec					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	1953	100.0	372	2 AAR27793	New platelet factor 4 receptor superfamily member PF4ARIi.	
2	1953	100.0	372	2 AAR68813	New platelet factor 4 receptor superfamily member PF4ARIi.	
3	1953	100.0	372	2 AAR92239	New platelet factor 4 receptor superfamily member PF4ARIi.	
4	1953	100.0	372	2 AAY06644	New platelet factor 4 receptor superfamily member PF4ARIi.	
5	1953	100.0	372	3 AAY90627	New platelet factor 4 receptor superfamily member PF4ARIi.	
6	1953	100.0	372	4 AAGB0124	New platelet factor 4 receptor superfamily member PF4ARIi.	
7	1953	100.0	372	6 ABPB1789	New platelet factor 4 receptor superfamily member PF4ARIi.	
8	1953	100.0	372	7 ADC22585	New platelet factor 4 receptor superfamily member PF4ARIi.	
9	1953	100.0	372	7 ADH14058	New platelet factor 4 receptor superfamily member PF4ARIi.	
10	1953	100.0	372	8 ADJ45761	New platelet factor 4 receptor superfamily member PF4ARIi.	
11	1953	100.0	372	8 ADP29199	New platelet factor 4 receptor superfamily member PF4ARIi.	
12	1953	100.0	372	8 ADR66972	New platelet factor 4 receptor superfamily member PF4ARIi.	
13	1953	100.0	378	4 ABB11873	New platelet factor 4 receptor superfamily member PF4ARIi.	
14	1947	99.7	372	3 AAY90661	New platelet factor 4 receptor superfamily member PF4ARIi.	
15	1947	99.7	372	7 ADC22719	New platelet factor 4 receptor superfamily member PF4ARIi.	
16	1947	99.7	372	7 ADH14192	New platelet factor 4 receptor superfamily member PF4ARIi.	
17	1638	83.9	374	8 ADP66969	New platelet factor 4 receptor superfamily member PF4ARIi.	
18	1635	83.7	374	2 AAY06643	New platelet factor 4 receptor superfamily member PF4ARIi.	
19	1635	83.7	374	8 ADQ29200	New platelet factor 4 receptor superfamily member PF4ARIi.	
20	1470	75.3	741	1 ABG19581	New platelet factor 4 receptor superfamily member PF4ARIi.	
21	635	32.5	368	2 AAW54371	New platelet factor 4 receptor superfamily member PF4ARIi.	
22	635	32.5	368	3 AAY90614	New platelet factor 4 receptor superfamily member PF4ARIi.	
23	635	32.5	368	4 AAGB0122	New platelet factor 4 receptor superfamily member PF4ARIi.	
24	635	32.5	368	6 ABPB1795	New platelet factor 4 receptor superfamily member PF4ARIi.	
25	635	32.5	368	7 AAE38602	New platelet factor 4 receptor superfamily member PF4ARIi.	
RESULT 1						
ID AAR27793	standard; protein; 372 AA.					
XX AAR27793;						
AC						
XX DT 25-MAR-2003 (revised)						
DT 12-MAR-1993 (first entry)						
DE New platelet factor 4 receptor superfamily member PF4ARIi.						
XX IL-8R; G-protein coupled receptor family; rhodopsin superfamily; pro-inflammatory cytokine; Brr.9.						
XX Homo sapiens.						
OS XX WO9217497-A1.						
PN XX WO9217497-A1.						
XX PD 15-OCT-1992.						
XX XX 23-MAR-1992; 92WO-US003317.						
PP PR 29-MAR-1991; 91US-00677211.						
XX PR 19-DEC-1991; 91US-00810782.						
PA (GETH) GENENTECH INC.						
XX PI Lee J, Holmes WE, Wood WI;						
XX XX WPI; 1992-366191/44.						
DR DR N-PSDB; AAQ37107.						
XX PS Claim 7; Fig 5 ; 78pp; English.						
XX CC The IL-8 receptor cDNA sequence was isolated (see AAQ3505) and a 874bp sub-fragment of the coding sequence was used as a probe to screen human cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two new gene sequences were found that are clearly related to the IL-8 receptor. One of these was contained in clone 8rr.9 and is predicted to encode an amino acid sequence which is 36% and 38% identical with the high and low affinity IL-8 receptor sequences, respectively. See also AAQ37107. (Updated on 25-MAR-2003 to correct PN field.)						
CC Sequence 372 AA;						

XX	WPI; 1995-283151/37.	PN	WO928468-A1.
DR	N-PSDB; AAQ99059.	XX	10-JUN-1999.
XX	New antibodies against interleukin 8 type B receptor - used to treat or prevent inflammation, also for detecting receptor expression and purification.	XX	02-DEC-1998;
PT		XX	98WO-US025561.
PR		XX	02-DEC-1997;
PT		XX	97US-00982493.
XX	Example 2; Col 49-52; 62pp; English.	PA	(RESC) UNIV CALIFORNIA.
XX	Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine receptor which was identified by probing cDNA libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See AAQ99066). (Updated on 25-MAR-2003 to correct PF field.)	XX	Modulating interaction of a Burkitt's Lymphoma Receptor 1 polypeptide and ligand, useful in drug screens.
CC	Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine receptor which was identified by probing cDNA libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See AAQ99066). (Updated on 25-MAR-2003 to correct PF field.)	XX	Claim 1; Page 38; 42pp; English.
CC	Sequence 372 AA;	XX	This sequence represents human Burkitt's lymphoma receptor 1 (BLR1). The invention relates to methods for modulating the interaction of BLR1 with its ligand, B lymphocyte chemoattractant (BLC, see AAY06642). The methods comprise combining BLR1 and BLC polypeptides with a candidate modulator agent under conditions whereby, but for the presence of the agent, the polypeptides engage in first interaction, and determining a second interaction of the polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the polypeptides. The modulator is preferably an antagonist, especially dominant negative, form of BLC. BLC and BLC agonists and antagonists may be useful for treating viral (e.g. HIV) infections, lymphoma, B lineage leukaemia, and autoimmune diseases such as rheumatoid arthritis, thyroiditis, and diabetes.
SQ	Query Match Score 1953; DB 2; Length 372; Best Local Similarity 100.0%; Pred. No 1.8e-196; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Sequence 372 AA;
Qy	1 MNYPITLEMDLENLDFWELDLDNYNDTSVLVENHLCPATGEPMLMASPKAVFVPAVSL 60	Qy	1 MNYPITLEMDLENLDFWELDLDNYNDTSVLVENHLCPATGEPMLMASPKAVFVPAVSL 60
Dy	1 MNYPITLEMDLENLDFWELDLDNYNDTSVLVENHLCPATGEPMLMASPKAVFVPAVSL 60	Dy	1 MNYPITLEMDLENLDFWELDLDNYNDTSVLVENHLCPATGEPMLMASPKAVFVPAVSL 60
Qy	61 IFLGVIGNVLVVILEREHQTRSSTEFLFLAVADLLVFILPAVABGSVGVWLGF 120	Qy	61 IFLGVIGNVLVVILEREHQTRSSTEFLFLAVADLLVFILPAVABGSVGVWLGF 120
Dy	61 IFLGVIGNVLVVILEREHQTRSSTEFLFLAVADLLVFILPAVABGSVGVWLGF 120	Dy	61 IFLGVIGNVLVVILEREHQTRSSTEFLFLAVADLLVFILPAVABGSVGVWLGF 120
Qy	121 LCKTVIALHKVNFKYCSSILLACIAYDRYLAIHVAVAYTHRRLISIHTTCGTIWLGFL 180	Qy	121 LCKTVIALHKVNFKYCSSILLACIAYDRYLAIHVAVAYTHRRLISIHTTCGTIWLGFL 180
Dy	121 LCKTVIALHKVNFKYCSSILLACIAYDRYLAIHVAVAYTHRRLISIHTTCGTIWLGFL 180	Dy	121 LCKTVIALHKVNFKYCSSILLACIAYDRYLAIHVAVAYTHRRLISIHTTCGTIWLGFL 180
Qy	181 ALPTEFLAKVSKQGHNNSLPRCTFSQENQAEATHAWFTSRFLYHAGFPLPMLVNGWCYVG 240	Qy	181 ALPTEFLAKVSKQGHNNSLPRCTFSQENQAEATHAWFTSRFLYHAGFPLPMLVNGWCYVG 240
Dy	181 ALPTEFLAKVSKQGHNNSLPRCTFSQENQAEATHAWFTSRFLYHAGFPLPMLVNGWCYVG 240	Dy	181 ALPTEFLAKVSKQGHNNSLPRCTFSQENQAEATHAWFTSRFLYHAGFPLPMLVNGWCYVG 240
Qy	241 VVHLRQAERPQOKAVRVALVTSIFLCLWSPHIUVFLDTIARLKAVDNTCKLNSL 300	Qy	241 VVHLRQAERPQOKAVRVALVTSIFLCLWSPHIUVFLDTIARLKAVDNTCKLNSL 300
Dy	241 VVHLRQAERPQOKAVRVALVTSIFLCLWSPHIUVFLDTIARLKAVDNTCKLNSL 300	Dy	241 VVHLRQAERPQOKAVRVALVTSIFLCLWSPHIUVFLDTIARLKAVDNTCKLNSL 300
Qy	301 PVAITMCBFFGLAHCCLNPMLTFAAGVKPRSDLSRLITKLGCTGPASLCQLFPSSRSSL 360	Qy	301 PVAITMCBFFGLAHCCLNPMLTFAAGVKPRSDLSRLITKLGCTGPASLCQLFPSSRSSL 360
Dy	301 PVAITMCBFFGLAHCCLNPMLTFAAGVKPRSDLSRLITKLGCTGPASLCQLFPSSRSSL 360	Dy	301 PVAITMCBFFGLAHCCLNPMLTFAAGVKPRSDLSRLITKLGCTGPASLCQLFPSSRSSL 360
Qy	361 SESENATSLTF 372	Qy	361 SESENATSLTF 372
Dy	361 SESENATSLTF 372	Dy	361 SESENATSLTF 372
RESULT 4		Qy	361 SESENATSLTF 372
AAY06644	standard; protein; 372 AA.	Dy	361 SESENATSLTF 372
XX		DB	361 SESENATSLTF 372
AC		DB	361 SESENATSLTF 372
XX		DB	361 SESENATSLTF 372
26-OCT-1999	(first entry)	DB	361 SESENATSLTF 372
DE	Human Burkitt's Lymphoma receptor 1 (BLR1).	DB	361 SESENATSLTF 372
XX	Burkitt's lymphoma receptor 1; BLR1; human; B lymphocyte chemoattractant; BLC; chemokine; ligand; drug screening; leukaemia; autoimmune disease; therapy.	DB	361 SESENATSLTF 372
OS	Homo sapiens.	DB	361 SESENATSLTF 372
		RESULT 5	AYY06627
			ID AAY90627 standard; protein; 372 AA.
			XX

AC PAA90627;	Db 121 LCKTVIALHKVNFYCSSILLACTAVDRYLAIYHVAHVAYRHRRLLSIHTCGTIVLWGVFL 180
XX DT 21-AUG-2000 (First entry)	Qy 181 ALPEILPAKVSQGHNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLYMGWCYVG 240
DB Human G protein-coupled receptor BLR1.	Db 181 ALPEILPAKVSQGHNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLYMGWCYVG 240
XX	
XX G protein-coupled receptor; GPCR; constitutively active;	Qy 241 VYHRLRQARQRORQAVRVALVTSIFFLCSYHIVFLDTLRLKAVDNTCKLNGSL 300
KW intramembrane loop 3; transmembrane domain 6; drug screening; agonist;	Db 241 VYHRLRQARQRORQAVRVALVTSIFFLCSYHIVFLDTLRLKAVDNTCKLNGSL 300
KW antagonist.	
XX OS Homo sapiens.	Qy 301 PVAITMCBFLGLAHCCINPMLYTAGVKFRSDLSRLITKLGCCTGPAISLCOLFPSPMRSSL 360
XX PN WO200022129-A1.	Db 301 PVAITMCBFLGLAHCCINPMLYTAGVKFRSDLSRLITKLGCCTGPAISLCOLFPSPMRSSL 360
XX	
PD 20-APR-2000.	Qy 361 SESENATSLTF 372
XX PP 12-OCT-1999; 99WO-US023938.	Db 361 SESENATSLTF 372
XX PR 13-OCT-1998; 98US-00170496.	
XX PA (AREN-) ARENA PHARM INC.	
XX PI Behan DP, Chalmers DT, Liaw CW;	RESULT 6 ID AAG80124 standard; protein; 372 AA.
XX DR WPI: 2000-329165/28.	XX AAG80124;
XX DR N-PSDB; AAA30626.	XX DT 17-JAN-2002 (first entry)
XX PR Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.	XX DE Human CXCR5 protein.
PT PT	XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
PT PR	XX KW Homo sapiens.
PT XX	XX OS Homo sapiens.
PT DR	XX PN WO200172830-A2.
PT XX	XX PD 04-OCT-2001.
PT DR	XX PF 02-APR-2001; 2001WO-EP003708.
PT DR	XX PR 31-MAR-2000; 2000DE-01016013.
PT XX	XX PA (IPFP-) IPF PHARM GMBH. (FORS-) FORSSMANN U.
PT XX	XX PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
PT DR	XX DR WPI: 2001-626256/72.
PT PR	XX PT Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
PT XX	XX Disclosure: Page 12-13; 26pp; German.
PS Sequence 372 AA:	PS CC This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in diseases. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic.
Qy Query Match 100.0%; Score 1953; DB 3; Length 372;	CC Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80045-AAG80128 represent human chemokine
Best Local Similarity 100.0%; Pred. No. 1..8e-196; Mismatches 0; Indels 0; Gaps 0;	CC
Matches 372; Conservative 1 MNYPATLEMPLENEDLFWEILDNYNDLQVLERHRQTRSSTETPLFHLLAVADLIVFILPFAVAGSGYGVWLCTF 60	CC
Db 1 MNYPATLEMPLENEDLFWEILDNYNDLQVLERHRQTRSSTETPLFHLLAVADLIVFILPFAVAGSGYGVWLCTF 60	CC
Qy 1 IFLLGIVGNVLYVLERHRQTRSSTETPLFHLLAVADLIVFILPFAVAGSGYGVWLCTF 120	CC
Db 61 IFLLGIVGNVLYVLERHRQTRSSTETPLFHLLAVADLIVFILPFAVAGSGYGVWLCTF 120	CC
Qy 121 LCKTVIALHKVNFYCSSILLACTAVDRYLAIYHVAHVAYRHRRLSIHTCGTIVLWGVFL 180	CC

CC fragments used to illustrate the method of the invention
 XX Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8E-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPITLLEMLENEDLFWFLDRLDNNTSLVENVHLCPATEGLMASPKAVTYPVAYSL 60
 DB 1 MNYPITLLEMLENEDLFWFLDRLDNNTSLVENVHLCPATEGLMASPKAVTYPVAYSL 60
 QY 61 IFLGQVIGNVLVLIERHQTRSTSTEFLFLAVADLLVFLPFAVAEGSYGVWLGT 120
 DB 61 IFLGQVIGNVLVLIERHQTRSTSTEFLFLAVADLLVFLPFAVAEGSYGVWLGT 120
 QY 121 LCKTVIALHKVNPFYCSSLIACIADVRLAIHVAVHAYHRRLSIHTTCGTIWLVGRI 180
 DB 121 LCKTVIALHKVNPFYCSSLIACIADVRLAIHVAVHAYHRRLSIHTTCGTIWLVGRI 180
 QY 181 ALPELTFAKYSQGHANNSPLRCTSQENQAEHTAWFPTSRFLYAGFLPMLMGWCVTG 240
 DB 181 ALPELTFAKYSQGHANNSPLRCTSQENQAEHTAWFPTSRFLYAGFLPMLMGWCVTG 240
 QY 241 VVHLRQAERPQRQAKARVAILTSIFLCSWYHIVFLDTLARLAVDNTCKLNSSL 300
 DB 241 VVHLRQAERPQRQAKARVAILTSIFLCSWYHIVFLDTLARLAVDNTCKLNSSL 300
 QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKPRSDLSRLITKLGCTGPASICQLFPSWRRSSL 360
 DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKPRSDLSRLITKLGCTGPASICQLFPSWRRSSL 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

DE Human CXCR chemokine receptor 5 protein SEQ ID NO:60.

XX ABP81789 standard; protein; 372 AA.
 AC ABP81789;
 DT 04-MAR-2003 (first entry)

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Cohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 XX 19-DEC-2001; 2001WO-US050107.
 PP 19-DEC-2000; 2000US-0257144P.
 PR Burmer GC, Roush CL, Brown JP;
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.

WPI; 2003-046718/04.
 DR N-PSDB; ABZ42633.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABP819 to ABP83619) of 12-24 amino acids. Also described: (1) a candidate polypeptide in a sample; (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, osteoarthritis, bacterial, fungal, protozoan or viral infections, osteoporosis, osteoarthritis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP81818, which are used in the exemplification of the present invention

XX Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8E-196; Mismatches 0; Indels 0; Gaps 0;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNYPITLLEMLENEDLFWFLDRLDNNTSLVENVHLCPATEGLMASPKAVTYPVAYSL 60
 DB 1 MNYPITLLEMLENEDLFWFLDRLDNNTSLVENVHLCPATEGLMASPKAVTYPVAYSL 60
 QY 61 IFLGQVIGNVLVLIERHQTRSTSTEFLFLAVADLLVFLPFAVAEGSYGVWLGT 120
 DB 61 IFLGQVIGNVLVLIERHQTRSTSTEFLFLAVADLLVFLPFAVAEGSYGVWLGT 120
 QY 121 LCKTVIALHKVNPFYCSSLIACIADVRLAIHVAVHAYHRRLSIHTTCGTIWLVGRI 180
 DB 121 LCKTVIALHKVNPFYCSSLIACIADVRLAIHVAVHAYHRRLSIHTTCGTIWLVGRI 180
 QY 181 ALPELTFAKYSQGHANNSPLRCTSQENQAEHTAWFPTSRFLYAGFLPMLMGWCVTG 240
 DB 181 ALPELTFAKYSQGHANNSPLRCTSQENQAEHTAWFPTSRFLYAGFLPMLMGWCVTG 240
 QY 241 VVHLRQAERPQRQAKARVAILTSIFLCSWYHIVFLDTLARLAVDNTCKLNSSL 300
 DB 241 VVHLRQAERPQRQAKARVAILTSIFLCSWYHIVFLDTLARLAVDNTCKLNSSL 300
 QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKPRSDLSRLITKLGCTGPASICQLFPSWRRSSL 360
 DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKPRSDLSRLITKLGCTGPASICQLFPSWRRSSL 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

RESULT 8
 ADC22585

Best Local Similarity 100.0%; Pred. No. 1.0e-196; N mismatches 0; Indels 0; Gaps 0;

QY 1 MNPYLTLEMLENLEDFWELDRDNNDTSVLVENHLCPATEGPMLMASFKAVFYPVDSL 60

Db 1 MNPYLTLEMLENLEDFWELDRDNNDTSVLVENHLCPATEGPMLMASFKAVFYPVDSL 60

QY 61 IFLILGVIGNYLVLVILERHRQTRSTTEFLHLAVADLILVFILPFVAFAGSGVWLGTF 120

Db 61 IFLILGVIGNYLVLVILERHRQTRSTTEFLHLAVADLILVFILPFVAFAGSGVWLGTF 120

QY 121 LCKTVIALHKVNFCSSLLACIAYDRLAIHVAYHRRLSITHITCGTIWLGFL 180

Db 121 LCKTVIALHKVNFCSSLLACIAYDRLAIHVAYHRRLSITHITCGTIWLGFL 180

QY 181 ALPEELPAKYSQGHNNSLPRCTPSQENQEATHAWPTSRFLYHAGFLPMLYNGWCYVG 240

Db 181 ALPEELPAKYSQGHNNSLPRCTPSQENQEATHAWPTSRFLYHAGFLPMLYNGWCYVG 240

QY 241 VVHLRQRQERPRORAKARVAVAILTISIFFLICMSPYHIVFLDTLARLKAVIDNTCKLNSSL 300

Db 241 VVHLRQRQERPRORAKARVAVAILTISIFFLICMSPYHIVFLDTLARLKAVIDNTCKLNSSL 300

QY 301 PVALTMCEPIGLAHCCNIPMLYTFAGVKERSDSLRLTFLGCTGPASLQLPPSWRRSSI 360

Db 301 PVALTMCEPIGLAHCCNIPMLYTFAGVKERSDSLRLTFLGCTGPASLQLPPSWRRSSI 360

QY 361 SESENATSLTTF 372

Db 361 SESENATSLTTF 372

RESULT 10

ID ADJ45761 standard; protein; 372 AA.

XX ADJ45761;

XX DT 06-MAY-2004 (first entry)

XX DE Human CXCR5 receptor, seq id 2.

XX KW Cardiovascular; cytostatic; respiratory; CNS; central nervous system;

KW gene therapy; haematological disease; cancer; cardiovascular disease;

KW respiratory disease; CXC chemokine receptor 5; CXCR5; human.

XX OS Homo sapiens.

XX XX WO2004015426-A1.

XX PD 19-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008141.

XX PR 06-AUG-2002; 2002EP-00017628.

XX PA (PARB) BAYER HEALTHCARE AG.

XX XX Golz S. Brueggemeier U, Summer H;

XX DR; 2004-191806/18.

XX N-PSDB; ADJ45760.

XX PT Screening for therapeutic agents, useful in diagnosing or treating hematological or cardiovascular diseases and cancer, comprises contacting a test compound with a CXC chemokine receptor 5 and determining activity.

XX Disclosure; SEQ ID NO 2; 131pp; English.

CC The invention relates to a method for screening for therapeutic agents useful in the treatment of haematological diseases, cancer, cardiovascular diseases, respiratory diseases and disorders of the peripheral and central nervous system in a mammal. The method of the

invention comprises contacting a test compound with a CXC chemokine receptor 5 (CXCR5) polypeptide or polynucleotide. The method of the invention is useful in screening for therapeutic agents that may be used in treating the diseases mentioned above. The regulators of a CXCR5 are useful for regulating CXCR5 activity or for preparing a pharmaceutical composition for the treatment of the stated diseases in a mammal. The method and compositions are also useful in diagnosing and treating the stated diseases. The current sequence represents the human CXCR5 receptor.

XX Sequence 372 AA;

	Query	Match	Score	Length	DB	Best Local Similarity	Matches	Pred. No.	Mismatches	Indels	Gaps
	QY	1 MNPYLTLEMLENLEDFWELDRDNNDTSVLVENHLCPATEGPMLMASFKAVFYPVDSL	100.0*	372	60	100.0*	372	0	0	0	0
	Db	1 MNPYLTLEMLENLEDFWELDRDNNDTSVLVENHLCPATEGPMLMASFKAVFYPVDSL	100.0*	372	60	100.0*	372	0	0	0	0
	QY	61 IFLILGVIGNYLVLVILERHRQTRSTTEFLHLAVADLILVFILPFVAFAGSGVWLGTF	100.0*	372	60	100.0*	372	0	0	0	0
	Db	61 IFLILGVIGNYLVLVILERHRQTRSTTEFLHLAVADLILVFILPFVAFAGSGVWLGTF	100.0*	372	60	100.0*	372	0	0	0	0
	QY	121 LCKTVIALHKVNFCSSLLACIAYDRLAIHVAYHRRLSITHITCGTIWLGFL	100.0*	372	60	100.0*	372	0	0	0	0
	Db	121 LCKTVIALHKVNFCSSLLACIAYDRLAIHVAYHRRLSITHITCGTIWLGFL	100.0*	372	60	100.0*	372	0	0	0	0
	QY	181 ALPEELPAKYSQGHNNSLPRCTPSQENQEATHAWPTSRFLYHAGFLPMLYNGWCYVG	100.0*	372	60	100.0*	372	0	0	0	0
	Db	181 ALPEELPAKYSQGHNNSLPRCTPSQENQEATHAWPTSRFLYHAGFLPMLYNGWCYVG	100.0*	372	60	100.0*	372	0	0	0	0
	QY	241 VVHLRQRQERPRORAKARVAVAILTISIFFLICMSPYHIVFLDTLARLKAVIDNTCKLNSSL	100.0*	372	60	100.0*	372	0	0	0	0
	Db	241 VVHLRQRQERPRORAKARVAVAILTISIFFLICMSPYHIVFLDTLARLKAVIDNTCKLNSSL	100.0*	372	60	100.0*	372	0	0	0	0
	QY	301 PVALTMCEPIGLAHCCNIPMLYTFAGVKERSDSLRLTFLGCTGPASLQLPPSWRRSSI	100.0*	372	60	100.0*	372	0	0	0	0
	Db	301 PVALTMCEPIGLAHCCNIPMLYTFAGVKERSDSLRLTFLGCTGPASLQLPPSWRRSSI	100.0*	372	60	100.0*	372	0	0	0	0
	QY	361 SESENATSLTTF 372	100.0*	372	60	100.0*	372	0	0	0	0
	Db	361 SESENATSLTTF 372	100.0*	372	60	100.0*	372	0	0	0	0

RESUL

T 11

AD029199 ID ADO29199 standard; protein; 372 AA.

XX AC ADO29199;

XX DT 29-JUN-2004 (first entry)

XX DE Human GPCR BLR1, SEQ ID NO:300.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimuscarinic; cytostatic; antiinflammatory; vasodilator; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antiborboce; viricide; hepatotropic; antibacterial; antinaemic; anorectic; dermatological; antiallergic; antithyroid; anorectic; nephrotoxic; gene therapy; GPCR modulator; human; immunosuppressive; receptor.

XX Homo sapiens.

PN XX	WO2004040000-A2.	QY	181 ALPPIFAKVSQGHANNSLPRCTTSQENOAEATHAWFTSRFLYHVAEGLIPMILVYNGWCVYG 240
PD 13-MAY-2004.		Db	181 ALPPIFAKVSQGHANNSLPRCTTSQENOAEATHAWFTSRFLYHVAEGLIPMILVYNGWCVYG 240
PF 09-SEP-2003;	2003WO-US028226.	QY	241 VVHLRQQRPRPQQAVRVALVTSIFLCLWCPHYHISFLDTLARLKAVDNTCKLNGSL 300
XX		Db	241 VVHLRQQRPRPQQAVRVALVTSIFLCLWCPHYHISFLDTLARLKAVDNTCKLNGSL 300
PR 09-SEP-2002;	2002US-0409303P.	QY	301 PVAITMCPEPLGLAHCCLNPMIYTFAVGKFRSDLSRLTLLKGCTPASLQLQFLPWRSSL 360
PR 09-APR-2003;	2003US-0461329P.	Db	301 PVAITMCPEPLGLAHCCLNPMIYTFAVGKFRSDLSRLTLLKGCTPASLQLQFLPWRSSL 360
XX	(PRIM-) PRIMAL INC.	QY	361 SESENATSLSTTF 372
XX	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;	Db	361 SESENATSLSTTF 372
PI Madisen L,	McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;	XX	
XX	DR; WPI; 2004-390329/36.	XX	
DR N-PSDB; ADO29818.		XX	
XX	Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunctions e.g. autoimmune diseases, angina pectoris, Parkinson's disease.	XX	
PS Claim 151; SEQ ID NO 300; 542pp; English.	The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	XX	
PS Claim 151; SEQ ID NO 300; 542pp; English.	The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	XX	
PS Sequence 372 AA;	Query Match 100 0%; Score 1953; DB 8; Length 372; Best Local Similarity 100.0%; Fred. No. 1.8e-196; Matches 372; Conservative 0; Mismatches 0; Gaps 0;	XX	
QY	1 MNYPLTLEMILENLDFWELDRDNNDTSVLENHLCPATEGDLMASPKAVFVPAVSL 60	CC	The present invention describes an isolated cancer associated (CA) nucleic acid (I). Also described: (1) an expression vector comprising (I) a microarray for detecting a CA nucleic acid; (4) an isolated cancer associated protein (CAP) polypeptide, encoded within an open reading frame of a CA sequence; (5) an isolated antibody, or its antigen binding fragment, that binds to the above polypeptide; (6) a hybridoma that produces the above monoclonal antibody; (7) a pharmaceutical composition comprising the above antibody and/or a pharmaceutical excipient; (8) a kit for detecting cancer cells, comprising the (monoclonal) antibody described above; (9) methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual; (10) a method for inhibiting growth of cancer cells in an individual; (11) a method for delivering a therapeutic agent to cancer cells in an individual; (12) an electronic library comprising the above polynucleotide or polypeptide, or
Db	1 MNYPLTLEMILENLDFWELDRDNNDTSVLENHLCPATEGDLMASPKAVFVPAVSL 60	CC	
QY	61 IFLLGYTGIVNVLVLIRHROTSSTEFLFLHAYADLLVFLPVAEGSVWLGTF 120	CC	
Db	61 IFLLGYTGIVNVLVLIRHROTSSTEFLFLHAYADLLVFLPVAEGSVWLGTF 120	CC	
QY	121 LCKTVIAHKVNFXCSSLLACIAYDRYLAIHVAYAHRRLSIIHTGTINLVGFLL 180	CC	
Db	121 LCKTVIAHKVNFXCSSLLACIAYDRYLAIHVAYAHRRLSIIHTGTINLVGFLL 180	CC	

their fragments; (13) methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CAP; (14) methods for detecting cancer associated with expression of a polypeptide in a test cell sample, or with the presence of an antibody in a test serum sample; (15) a method for treating cancers; and (16) a method for inhibiting the expression of CA gene in a cell. The CA sequences have cytosolic activity, and can be used in vaccines, and in gene therapy. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. They may also be used in screening for agents that modulate cancer. The present sequence represents a cancer associated protein (CAP) sequence, which is used in the exemplification of the present invention.

Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 8; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.be-196; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Db 1 MNYPITLEMDLENEDLFWELDRDNYNDTSVLVHNLCPATEGPLMASPKAVFVPAVSL 60

Db 1 MNYPITLEMDLENEDLFWELDRDNYNDTSVLVHNLCPATEGPLMASPKAVFVPAVSL 60

Qy 61 IFLUGVIGNVLYLVEHROTRSTSSTEFLHLAVADLLVFLPFAVAGSGVWLGTF 120

Db 61 IFLUGVIGNVLYLVEHROTRSTSSTEFLHLAVADLLVFLPFAVAGSGVWLGTF 120

Qy 121 LCKTVIALLKVNFCSSLLACIADVRLAIVHVAHTRRLLSIHTTCGTIWLVLGTL 180

Db 121 LCKTVIALLKVNFCSSLLACIADVRLAIVHVAHTRRLLSIHTTCGTIWLVLGTL 180

Qy 181 ALPELFALKVSGQHHNNSPRCTEFSQENQAEATHAWFTSRFLYIVAGFLPMLVNGWCYVG 240

Db 181 ALPELFALKVSGQHHNNSPRCTEFSQENQAEATHAWFTSRFLYIVAGFLPMLVNGWCYVG 240

Qy 241 VVHLRQAQRPRQPKAVVALVLTISFLCSPYHIVFLDTLARKAVDNTCKLNSL 300

Db 241 VVHLRQAQRPRQPKAVVALVLTISFLCSPYHIVFLDTLARKAVDNTCKLNSL 300

Qy 301 PVAITMCBPFGLAHCLNPMLYTAGVIFKPSDSLRLTFLGCTGPASLQLQFLPSWRSSL 360

Db 301 PVAITMCBPFGLAHCLNPMLYTAGVIFKPSDSLRLTFLGCTGPASLQLQFLPSWRSSL 360

Qy 361 SESENATSLTTF 372

Db 361 SESENATSLTTF 372

RESULT 13

ABB11873 standard; peptide; 378 AA.

XX

AC ABB11873;

XX DT 11-JAN-2002 (first entry)

Human Burkitt lymphoma receptor homologue, SEQ ID NO:2243.
 Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasoconstrictor; cardiotonic; virucide; antibacterial; fungicidal; antiviral; antilulcer.

Homo sapiens.

CC	XX	W0200157188-A2.
CC	PN	W0200157188-A2.
CC	XX	09-AUG-2001.
CC	XX	05-FEB-2001; 2001WO-US003800.
CC	PP	03-FEB-2000; 2000US-00496914.
CC	PR	27-APR-2000; 2000US-00560875.
CC	XX	(HYSE-) HYSEQ INC.
CC	PA	
CC	PI	Tang YT, Liu C, Drmanac RT;
CC	XX	
SQ	XX	WPI; 2001-457740/49.
	DR	DR-N-PSDB; ABA09117.
	XX	Human proteins and DNA encoding sequences useful for preventing, treating and ameliorating a medical condition in a mammalian subject e.g. arthritis.
	PT	
	PT	
	PT	
	XX	Claim 20: Page 269; 1963pp; English.
	PS	
	XX	Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibitor- or ligand activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.
	CC	depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
	CC	Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
	SQ	Sequence 378 AA;
	XX	Query Match Best Local Similarity Score 1953; DB 4; Length 378; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MNYPITLEMDLENEDLFWELDRDNYNDTSVLVHNLCPATEGPLMASPKAVFVPAVSL 60	
Db	7 MNYPITLEMDLENEDLFWELDRDNYNDTSVLVHNLCPATEGPLMASPKAVFVPAVSL 66	
Qy	61 IFLUGVIGNVLYLVEHROTRSTSNETFLHLAVADLLYFLPPAVAESGVWLGTF 120	
OS	Homo sapiens.	

Db	67	IPLIGVIGNVLVLYLIERHQTRSSTETFLHLAVADLLVFIILPAVEGSGVWLGF	T 128
Qy	121	LCKTVALHKVNFYCSLLIACIATDYLAIHVAYHAYRHLISLHTITCGTIVLVGFLL	180
Db	127	LCKTVALHKVNFYCSLLIACIATDYLAIHVAYHAYRHLISLHTITCGTIVLVGFLL	186
Db	161	ALPILFLAKYVSGHHNNSLPRCTFEQQENQETHAFTSRELYHVGFLFPMVMWCVYG	240
Qy	187	ALPILFLAKYVSGHHNNSLPRCTFEQQENQETHAFTSRELYHVGFLFPMVMWCVYG	246
Qy	241	VVHLRQAQRPQKAVRVAILTVSIPFLCWSPHIVIPFLDTLARLKAVDNTCLNGSL	300
Db	247	VVHLRQAQRPQKAVRVAILTVSIPFLCWSPHIVIPFLDTLARLKAVDNTCLNGSL	306
Qy	301	PVAITMCEBFGLAHICLNPNMLYTFAGVKFRSDLSRLTTKGCTGPASLCOLFPSPRSSL	360
Db	307	PVAITMCEBFGLAHICLNPNMLYTFAGVKFRSDLSRLTTKGCTGPASLCOLFPSPRSSL	366
Qy	361	SESENATSLTTF	372
Db	367	SESENATSLTTF	378
RESULT 14			
	AAY90661		
ID	AAY90661	standard; protein:	372 AA.
XX			
AC	AAY90661;		
XX			
DT	21-AUG-2000	(first entry)	
XX			
DE	Human mutant G protein-coupled receptor BLR1. (V258K).		
XX			
KW	G protein-coupled receptor; GPCR; constitutively active;		
KW	intramembrane loop 3; mutine;		
KW	agonist; mutant; mutine.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO20022129-A1.		
XX			
PD	20-APR-2000.		
XX			
PF	12-OCT-1999;	99WO-US023938.	
XX			
PR	13-OCT-1998;	98US-00170496.	
XX			
PA	(AREN-) ARENA PHARM INC.		
XX			
Behan DP,	Chalmers DT,	Liau CW;	
XX			
DR	WPI; 2000-3232165/28.		
DR	N-PSDB; AAA30327.		
XX			
PT	Non-endogenous constituents activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.		
PT			
XX			
PS	Example 2, Page 254-256; 341PP; English.		
XX			
CC	The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90663-AAY90677 and AAY90683-190687), and to DNA encoding them (AAA30799-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be		

CC	non-endogenous, or a mixture of endogenous and non-endogenous
CC	antagonists. The constitutively active GPCRs are useful for identifying
CC	agonists, antagonists and partial agonists for use as pharmaceutical
CC	agents. The mutant proteins are also useful in research settings for
CC	elucidating the roles of the receptors in normal and diseased conditions.
CC	Antagonists for a particular GPCR are useful for treating diseases and
CC	disorders associated with that receptor. Because the novel mutant GPCRs
CC	are constitutively active, they can be used directly for screening of
CC	compounds without the need for endogenous ligands. Sequences AAY90643-
CC	AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
XX	Sequence 372 AA:
SQ	<pre> Query Match 99.7%; Score 1947; DB 3; Length 372; Best Local Similarity 99.7%; Pred. No. 7.5e-196; Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 MNYPFLMDEMILENLDLFWEDLRDLYNDNTSLVENHLCPATGPFLMASFKAVFVPAVAYSL 60 Db 1 MNYPFLMDEMILENLDLFWEDLRDLYNDNTSLVENHLCPATGPFLMASFKAVFVPAVAYSL 60 Qy 61 IFLLGVIGNVLVILERHQTRSSSETELPHLAYADLLVYFILDPAVAGSGVNLYGTF 120 Db 61 IFLLGVIGNVLVILERHQTRSSSETELPHLAYADLLVYFILDPAVAGSGVNLYGTF 120 Qy 121 LCKTVTAHKVNFYCSSLACIAYDRYLAIHVAYHAYRRLLSITHTCGTIWLGVLL 180 Db 121 LCKTVTAHKVNFYCSSLACIAYDRYLAIHVAYHAYRRLLSITHTCGTIWLGVLL 180 Qy 181 ALPEYIAFKVSQGHINSLPRCTFSCENOQAETHAFTSRELYHAGFLLPMLVMGCYVG 240 Db 181 ALPEYIAFKVSQGHINSLPRCTFSCENOQAETHAFTSRELYHAGFLLPMLVMGCYVG 240 Qy 241 VVHRRLQAQRPRQRKAVRVALVTISIFFCLCWSPTIVIFDTLARKAVDNTCKLNGSL 300 Db 241 VVHRRLQAQRPRQRKAVRVALVTISIFFCLCWSPTIVIFDTLARKAVDNTCKLNGSL 300 Qy 301 PVAITMCFFGLAHCCLNPMLYTFAQVKPFSDLSRLULTGCTGPAISLCQLPPSWSRSSL 360 Db 301 PVAITMCFFGLAHCCLNPMLYTFAQVKFRSDLSSRLTKGCTGPAISLCQLPPSWSRSSL 360 Qy 361 SESENATSTTFF 372 Db 361 SESENATSLTTFF 372 </pre>
RESULT 15	
ID	ADC22719 standard; protein: 372 AA.
XX	
AC	ADC22719;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human G protein-coupled receptor (GPCR) polypeptide #58.
XX	
KW	G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
KW	intracellular-3 region; IC3; receptor.
XX	
OS	Homo sapiens.
XX	
PN	US6555339-B1.
XX	
PD	29-APR-2003.
XX	
PP	98US-00170496.
XX	
PR	14-APR-1997; 97US-00834449.
PR	14-APR-1998; 98US-0006188.
PR	26-JUN-1998; 98US-009073P.
PR	07-AUG-1998; 98US-0095677P.
XX	(AREN-) ARENA PHARM INC.

XX Liaw CW, Behan DP, Chalmers DT;
 XX DR WPI: 2003-742861/70.
 XX N-PSDB; ADC2218.

XX Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for constitutive activity.

XX Example 2: SEQ ID NO 200; 221pp; English.

CC The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCRs, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the invention.

XX SQ Sequence 372 AA:

	Query Match	Score	Length	DB	Best Local Similarity	Pred.	No.	Matches	Mismatches	Indels	Gaps
Qy	1	99.7%	372	DB	99.7%	7.5e-196	0;	371;	0;	0;	0;
Db	1	99.7%	372	DB	99.7%	7.5e-196	0;	371;	0;	0;	0;
Qy	61	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	61	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	61	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	61	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	121	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	121	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	181	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	181	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	241	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	241	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	301	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	301	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Qy	361	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;
Db	361	1	1947	DB	99.7%	7	0;	371;	0;	0;	0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:47:36 ; Search time 41 Seconds
(without alignments)
872.991 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPTLLEMILENLDFWE.....PSWRRSSLSESENATSLRTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79;*
1: p1r1;*
2: p1r2;*
3: p1r3;*
4: p1r4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	372	2 S26667	G protein-coupled MDPR5 protein - h
2	1700	87.0	327	2 S42628	G protein-coupled G protein-coupled
3	1635	83.7	374	2 S32275	G protein-coupled interferon- inducible
4	1590	81.4	374	2 JB0349	interleukin-8 recep-
5	615	31.5	367	2 A53611	lymphocyte-specific
6	601.5	30.8	360	2 B55275	G protein-coupled
7	596	30.5	378	2 A53732	G protein-coupled
8	574	29.4	378	2 A45680	G protein-coupled
9	571.5	29.3	378	2 A55735	interleukin-8 recep-
10	569	29.1	355	2 JQ1231	interleukin-8 recep-
11	561	28.7	350	2 A39445	interleukin-8 recep-
12	547	28.0	358	2 A53732	interleukin-8 recep-
13	543	27.8	352	2 G00048	fusin (LESTR) - c
14	537.5	27.6	352	2 JC4577	neuropeptide Y/pep
15	537.5	27.5	353	2 S28757	neuropeptide Y/pep
16	536	27.4	356	2 S42086	interleukin-8 recep-
17	519.5	26.6	359	2 A48921	interleukin-8 recep-
18	499.5	25.6	354	2 A23669	interleukin-8 recep-
19	497	25.4	355	2 JC5087	G protein-coupled
20	495.5	25.4	360	2 JC4587	chemokine (C-C) re-
21	494.5	25.3	369	2 JC5068	G protein-coupled
22	479.5	24.6	360	2 A57160	chemokine (C-C) re-
23	474	24.3	355	2 A49339	macrophage inflam-
24	465	23.8	360	2 JC2443	chemokine (C-C) re-
25	461.5	23.6	354	2 I58186	probable G protein
26	461.5	23.6	374	2 I3850	chemokine (C-C) re-
27	461	23.6	352	2 A43113	chemokine (C-C) re-
28	455	23.3	355	2 A45177	chemokine (C-C) re-
29	450	23.0	383	2 S55594	G protein-coupled

ALIGNMENTS

RESULT 1
S26667
G protein-coupled receptor BLR1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S26667
R;Dobner, T.; Wolf, I.; Enrich, T.; Lipp, M.
Bur. J. Immunol. 22, 2795-2799, 1992
A;Title: Differentiation-specific expression of a novel G protein-coupled receptor frc
A;Reference number: S26667; PMID: 1425907
A;Accession: S26667
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <DB>
A;Cross-references: UNIPROT:P32302; EMBL:X68149; PIDN:CAA48252.1; PID:9294
A;Gene: GDB:BLR1
A;Cross-references: GDB:136235; OMIM:601613
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match Score 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.7e-162; Mismatches 0; Indels 0; Gaps 0;

Match	Score	Length	Start	End	Mismatches	Indels	Gaps
Match	1	100.0	1	372	0	0	0
Match	2	100.0	1	372	0	0	0
Match	3	100.0	1	372	0	0	0
Match	4	100.0	1	372	0	0	0
Match	5	100.0	1	372	0	0	0
Match	6	100.0	1	372	0	0	0
Match	7	100.0	1	372	0	0	0
Match	8	100.0	1	372	0	0	0
Match	9	100.0	1	372	0	0	0
Match	10	100.0	1	372	0	0	0
Match	11	100.0	1	372	0	0	0
Match	12	100.0	1	372	0	0	0
Match	13	100.0	1	372	0	0	0
Match	14	100.0	1	372	0	0	0
Match	15	100.0	1	372	0	0	0
Match	16	100.0	1	372	0	0	0
Match	17	100.0	1	372	0	0	0
Match	18	100.0	1	372	0	0	0
Match	19	100.0	1	372	0	0	0
Match	20	100.0	1	372	0	0	0
Match	21	100.0	1	372	0	0	0
Match	22	100.0	1	372	0	0	0
Match	23	100.0	1	372	0	0	0
Match	24	100.0	1	372	0	0	0
Match	25	100.0	1	372	0	0	0
Match	26	100.0	1	372	0	0	0
Match	27	100.0	1	372	0	0	0
Match	28	100.0	1	372	0	0	0
Match	29	100.0	1	372	0	0	0

Query Match Score 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.7e-162; Mismatches 0; Indels 0; Gaps 0;

Match	Score	Length	Start	End	Mismatches	Indels	Gaps
Match	1	100.0	1	372	0	0	0
Match	2	100.0	1	372	0	0	0
Match	3	100.0	1	372	0	0	0
Match	4	100.0	1	372	0	0	0
Match	5	100.0	1	372	0	0	0
Match	6	100.0	1	372	0	0	0
Match	7	100.0	1	372	0	0	0
Match	8	100.0	1	372	0	0	0
Match	9	100.0	1	372	0	0	0
Match	10	100.0	1	372	0	0	0
Match	11	100.0	1	372	0	0	0
Match	12	100.0	1	372	0	0	0
Match	13	100.0	1	372	0	0	0
Match	14	100.0	1	372	0	0	0
Match	15	100.0	1	372	0	0	0
Match	16	100.0	1	372	0	0	0
Match	17	100.0	1	372	0	0	0
Match	18	100.0	1	372	0	0	0
Match	19	100.0	1	372	0	0	0
Match	20	100.0	1	372	0	0	0
Match	21	100.0	1	372	0	0	0
Match	22	100.0	1	372	0	0	0
Match	23	100.0	1	372	0	0	0
Match	24	100.0	1	372	0	0	0
Match	25	100.0	1	372	0	0	0
Match	26	100.0	1	372	0	0	0
Match	27	100.0	1	372	0	0	0
Match	28	100.0	1	372	0	0	0
Match	29	100.0	1	372	0	0	0

Query Match Score 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.7e-162; Mismatches 0; Indels 0; Gaps 0;

Match	Score	Length	Start	End	Mismatches	Indels	Gaps
Match	1	100.0	1	372	0	0	0
Match	2	100.0	1	372	0	0	0
Match	3	100.0	1	372	0	0	0
Match	4	100.0	1	372	0	0	0
Match	5	100.0	1	372	0	0	0
Match	6	100.0	1	372	0	0	0
Match	7	100.0	1	372	0	0	0
Match	8	100.0	1	372	0	0	0
Match	9	100.0	1	372	0	0	0
Match	10	100.0	1	372	0	0	0
Match	11	100.0	1	372	0	0	0
Match	12	100.0	1	372	0	0	0
Match	13	100.0	1	372	0	0	0
Match	14	100.0	1	372	0	0	0
Match	15	100.0	1	372	0	0	0
Match	16	100.0	1	372	0	0	0
Match	17	100.0	1	372	0	0	0
Match	18	100.0	1	372	0	0	0
Match	19	100.0	1	372	0	0	0
Match	20	100.0	1	372	0	0	0
Match	21	100.0	1	372	0	0	0
Match	22	100.0	1	372	0	0	0
Match	23	100.0	1	372	0	0	0
Match	24	100.0	1	372	0	0	0
Match	25	100.0	1	372	0	0	0
Match	26	100.0	1	372	0	0	0
Match	27	100.0	1	372	0	0	0
Match	28	100.0	1	372	0	0	0
Match	29	100.0	1	372	0	0	0

Db 361 SESENATSLTTF 372

A;Cross-references: GB:L20312; NID:g438798; PIDN:AAA16852.1; PID:g438799
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

RESULT 2

SS6162 MDCR15 protein - human
 C;Species: Homo sapiens (man)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
 C;Accession: SS6162
 R;Barela, L.; Loettger, M.; Tobler, A.; Baggioletti, M.; Moser, B.
 Biochem. J. 309, 773-779, 1995
 A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
 A;Reference number: SS6162; MUID:93366931; PMID:7639692
 A;Accession: SS6162
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-372 <BAR>
 A;Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
 C;Superfamily: vertebrate rhodopsin

Query Match Score 87.0%; Pred. No. 1.6e-140; Length 327;
 Best Local Similarity 99.7%; Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 46 MASFKAVFVPAVYLSLFLFGIVNYLVILVERHQTTSSTETFLFHLLAVADLLVFLP 105
 Db 1 MASFKAVFVPAVYLSLFLFGIVNYLVILVERHQTTSSTETFLFHLLAVADLLVFLP 60

Qy 106 FAVAEGSGVNVLGTFELCKTVITALHKNFYCSSLLIACIAYDRYLAIHVAYHRRRLS 165
 Db 61 FAVAEGSGVNVLGTFELCKTVITALHKNFYCSSLLIACIAYDRYLAIHVAYHRRRLS 120

Qy 166 IHTCGTIIWVGFLLALPELFKAVYSGQHINNSLPRCTSQENQAETHWFTSRFLHYA 225
 Db 121 IHTCGTIIWVGFLLALPELFKAVYSGQHINNSLPRCTSQENQAETHWFTSRFLHYA 180

Qy 226 GFLPLPMVMECRCYGVVHLRQLAQQRPKQRAVRYAILVLYTISIFFLCWSPYHIVFLDTIA 285
 Db 181 GFLPLPMVMECRCYGVVHLRQLAQQRPKQRAVRYAILVLYTISIFFLCWSPYHIVFLDTIA 240

Qy 286 RLKAVDNTCKLNGSLSPVAVITMCCEFGLAHCCLNPNMLYTFAVGKFRSDLSRLTLTKLGCTGP 345
 Db 241 RLKAVDNTCKLNGSLSPVAVITMCCEFGLAHCCLNPNMLYTFAVGKFRSDLSRLTLTKLGCTGP 300

Qy 346 ASLCQLPSPVRSSESENATSLTTF 372
 Db 301 ASLCQLPSPVRSSESENATSLTTF 327

RESULT 4

S32785 G protein-coupled receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Dec-1993 #Sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S32785
 R;Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
 FEBS Lett., 321, 173-178, 1993
 A;Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is express
 A;Reference number: S32785; MUID:83238948; PMID:8386678
 A;Accession: S32785
 A;Molecule type: mRNA
 A;Residues: 1-374 <KOU>
 A;Cross-references: UNIPROT:P34997; GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

RESULT 3

S42628 G protein-coupled receptor Gpcr6 - mouse
 N;Alternate names: interleukin-8 receptor homolog; mUBLR1 protein
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C;Accession: S42628; C44909
 R;Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.
 Eur. J. Immunol. 23, 2522-2539, 1993
 A;Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation
 A;Reference number: S42628; MUID:9400911; PMID:8405054
 A;Accession: S42628
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-374 <KA>
 A;Cross-references: UNIPROT:Q04683; EMBL:X71788; NID:92598563; PIDN:CAA50673.1; PID:g433
 R;Willkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
 Genomics 18, 175-184, 1993
 A;Title: Identification, chromosomal location, and genome organization of mammalian G-pro
 A;Reference number: A48809; MUID:94116380; PMID:8288218
 A;Accession: C48809
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Accession: 151-269 <WIL>
 A;Residues: 151-269 <WIL>

Qy 239 VGVVHRLRQARRPQRQAVRAVAILVTTIFLCNSPYHVIVFLDTLARLKAVDNTCKLNG 298
 Db 241 VGVERLQLQQRPRQRQAVRAVAILVTTIFLCNSPYHVIVFLDTLARLKAVDNTCKLNG 300
 A;Status: preliminary
 A;Accession: I38712
 A;Molecule type: mRNA
 A;Residues: 1-15 <RE2>
 A;Cross-references: EMBL:U11872; NID:9511808; PID:4511809; EMBL:U11878; NID:9511810; PID:4511817; EMBL:U11879; NID:9511818; PID:4511819; EMBL:U11876; R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
 J. Biol. Chem. 269, 11065-11072, 1994
 A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor
 A;Reference number: A53611; MUID:9420927; PMID:7512557
 A;Accession: A53611
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 6-360 <SPR>
 A;Cross-references: GB:MM99412; GB:L19593
 R;Murphy, P.M.; Tiffany, H.L.
 Science 253, 1280-1283, 1991
 A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
 A;Reference number: A39446; MUID:91168200; PMID:1891716
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 6-360 <MTR>
 A;Cross-references: GB:MT73969
 C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
 C;Genetics:
 A;Gene: GDB:IL8RB; IL8RA
 A;Cross-references: GDB:127868; OMIM:146928
 A;Map position: 2q35-2q35
 C;Superfamily: vertebrate rhodopsin
 C;Protein family: G protein-coupled receptor; transmembrane protein
 Query Match 31.5%; Score 615; DB 2; Length 367;
 Best Local Similarity 38.8%; Pred. No. 5.7e-46;
 Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;
 Qy 28 NDTSVNEHILCPATEGPMLMASFKAVFVPPVAYSLIFLIGVGNVLYLVLLERHQRTSSTB 87
 Db 32 NESDFSDSPPCPQ---DFSUNFDRTFLPAPLSSFLIGLNGAVAAVLSQRTAASSD 88
 Qy 88 TFLPHLAVADLLYFLIPPAVEAGSGVWFLGFLICKTVAALKHNCNYCSLILACTIAVDR 147
 Db 89 TFLHLAVADVLVLTLPDWAQDAVQWFGPGFLICKVAGALNINFYGAFLACISDR 148
 Qy 148 YLAIVHAYAHYRHLRLLSIHTCTGTIWLVGFLLALPELFKAVSQGHNNSLPRCTPSQE 207
 Db 149 YLSIVHATQIYRDRPVRYALVTCIUVKGCLLPALPDFTYLSDANYDQLINA-THCQYNNP 207
 Qy 208 NQAEHTHAWPTSRFLYHVAGFLPMLVMGNCYVGVYHRIRQAQRPQRKAVALVTSI 267
 Db 208 QVGRT-- ALRVQLQVAFLLPLVMMACYAHLLAVL-LVSRGQRPRAMRLVVVVA 262
 Qy 268 FFRLWSPYHVIVFLDTLARLKAVDNTCKLNGSFVPAITMCEFLGLAHCCLNPMLYTPAGV 327
 Db 263 FAVCWTPHVLVLDIMDVGVLARNCGRESHVDAKSSTSFGYMGCCLNPLUYAFGV 322
 Qy 328 KFRSDLSLRLLTKLGET--GPASLQQLPFSWRRSSLSESENATSL 369
 Db 323 KFREQMWMFLTRLGSDORGQPR--QPSSSRRESSWSETTEASYL 365
 RESULT 6
 A53611 Interleukin-8 receptor type B - human
 C;Species: Homo sapiens (man)
 C;Dte: 07-Oct-1994 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
 C;Accession: I37898; I38712; A53611; A39446
 R;Ahluia, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B
 A;Reference number: I37898; MUID:95014476; PMID:7922358
 A;Accession: I37898
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-360 <RES>
 A;Cross references: UNIPROT:P25025; EMBL:U11869; NID:9511801; PID:60656.1; PID:9511809; EMBL:U11870; NID:9511808; PID:AAA64380.1; PID:4511809; EMBL:U11872; NID:9511810; PID:4511817; EMBL:U11877; NID:9511818; PID:4511819; EMBL:U11878; R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
 J. Biol. Chem. 269, 11065-11072, 1994
 A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor
 A;Reference number: A53611; MUID:9420927; PMID:7512557
 A;Accession: A53611
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 6-360 <SPR>
 A;Cross-references: GB:MM99412; GB:L19593
 R;Murphy, P.M.; Tiffany, H.L.
 Science 253, 1280-1283, 1991
 A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
 A;Reference number: A39446; MUID:91168200; PMID:1891716
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 6-360 <MTR>
 A;Cross-references: GB:MT73969
 C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
 C;Genetics:
 A;Gene: GDB:IL8RB; IL8RA
 A;Cross-references: GDB:127868; OMIM:146928
 A;Map position: 2q35-2q35
 C;Superfamily: vertebrate rhodopsin
 C;Protein family: G protein-coupled receptor; transmembrane protein
 Query Match 30.8%; Score 601.5; DB 2; Length 360;
 Best Local Similarity 38.6%; Pred. No. 8.4e-45;
 Matches 141; Conservative 57; Mismatches 154; Indels 13; Gaps 8;
 Qy 9 MDILENDLFWELDLDNYNDTSVLVENHILCPATE-GPLMASFKAVFVPAVSVLFLIGV 67
 Db 6 MESDFED-FWKGEDSLNSYSSTSTPPFLDAAPCEESLEINKYFVVTIYALVELLSSL 64
 Qy 68 GNVLVLYTLERHQRTSSTFLFHLLAVDLVLFILPFAVEAGSVGRWLGFLCKTVTA 127
 Db 65 GNSLVMVLVLSRGSRGSVTDVLLNLADLFLATLPPIAWSKNGWIFGFLCKRVSL 124
 Qy 128 LHKNVNFCSSILLACIAAVDRYLAIVAHVAYHRRLSITHITCGTINIUGFLILALPBLIF 187
 Db 125 LKEVNFNFGSILLACISVDRYLAIVAHATRILTKQRKYL-VKFICLTSINGLSSLLALPVLIF 183
 Qy 188 AKVSGQEHANSILSPCTFSQENOAEHAW-FITSRFLVHAGFLLPMLVMGWCTYGVVHRL 246
 Db 184 RTTV--YSSNTSPACYEDMGN--NTANWRMLLRLPQSFGFIVPLTIMLCYGETLRTL 239
 Qy 247 QFQRPRQRKAVRVALVTSIFFLMSPYHIVFLDYLARLKAVDNTCKLNGSLPVALT 306
 Db 240 KA-HMGOKHMRMVIVAVFLPLVLPNVLQIADLMRTQVIQETCERNHIDRALDA 298
 Qy 367 TSLT 371
 Db 355 HTST 359
 RESULT 7
 B55735 Lymphocyte-specific G protein-coupled receptor EB1 - human
 N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
 C;Species: Homo sapiens (man)
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C;Accession: B55735; SS2443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SCH>
A;Cross-references: UNIPROT:P32248; GB:L31581; NID:9468319; PID:9468320
R;Burgtstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transcribed to the EMBL Data Library, February, 1995
A;Reference number: S52443
A;Accession: S52443
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342055; OMIM:600242
A;Map position: 17q1-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match Score 596; DB 2; Length 378;
Best Local Similarity 36.8%; Pred. No. 2.7e-44;
Matches 129; Conservative 77; Mismatches 123; Indels 22; Gaps 9;

Qy 29 DTSLVENVHLCPATGGLMASFKAVFVPAVAYSLIFLGVIGNVLVILVERHRROTSSRET 88
Db 40 DYLPEFS-LCSKD---VRNFKAWFLPIMMSIICPGDNGNLVLTLYPKRLKTMDDT 95

Qy 89 FLPLHAVADLLVFLPFAVAGSGVWNLGTFLECKTVIALHKVNKFYCSSLLACIADVRY 148
Db 96 YLLNLAVIDDLFLTLTPWAVSAAKSWVPSVHECKLFLAFYKNSFFSGMLLCLISIRY 155

Qy 149 LAIVAHAVAYRHRR--LLSHITCGTIVLGVFLALPELFPAVYSQGHNNSLPRCTPSQ 206
Db 156 VAIVQAVSAHRARVLLSKLSCVGWIWILATLSIPEELYSDQRSSSEQAM-RCSLJIT 214

Qy 207 ENOAETHAWFTSRFLYHVAGFLPMLVWGVYVHLRQAORPQAVRYVAILVTS 266
Db 215 EH---VEAFTIQAQMVIGFLVLLSPASLQLQFPWS---RSSLS-ESENATSLT 370

Qy 267 IFPLCWSPYHIVFLDTLARLKAVDNTCKLNGSLPVAVITMCEFLGLAAGCCLNPMLYTAG 326
Db 271 VFIVFQLPYNGVVAQTAVANFNITSSTCELSKOLNIAVDTVSACRVCCNPFYATIG 330

Qy 327 VKFRDLSRLTJKUGCTGPASLQLQFPWS---RSSLS-ESENATSLT 370
Db 331 VKFRNDLFLKFDLGCLSQEQLRQ---WSSCRHIRSSMSVEATTTIFS 377

RESULT 9
A55735
A;Cross-references: UNIPROT:P47774; GB:L31580; NID:9468340; PID:9468321; PID:9468348;
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #Sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; PMID:95154835; PMID:7851893
A;Accession: A55735
A;Molecule type: mRNA
A;Residues: 1-378 <SCB>
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match Score 571.5; DB 2; Length 378;
Best Local Similarity 36.7%; Pred. No. 3.6e-42; Mismatches 71; Indels 129; Gaps 4;

Qy 48 SPKAVFVPAVAYSLIFLGVIGNVLVILVERHRROTSSRETFLFLAVADLLVFLPFA 107
Db 55 NFYAWFLPMYSTCFGLGNCLVHHTTYPERFLKMTDTYLNLAVIDDLFLPLPFW 114

Qy 108 VAEGSVGFLVGLFLCRVIALHKVNKFYCSSLLACIADVRYHAYRHR--LIS 165
Db 115 AYSEAKSMFVGYVLLKGKFGIYKLSPSGMLLCLISDRYAVQAVSRHRHARVLLI 174

Qy 166 IHTCGTIVLGVFLALPELFPAVYSQGHNNSLPRCTFSQENAEHTAWFTSRFLYHVA 225
Db 175 SKLSCVGTVMLALFLSIPELLYSGLQNSGEDT-RESLV--SAQVDALEITVQAVQMPF 230

Qy 226 GFLPMLVMGWCYVGFVYVHLRQAORPQAVRYVAILVTSIFFLCWSPYHIVFLDTLA 285
Db 231 GFLPMLAMSFSCYLIITRTLLQ-RNFERNAKIAKVIIAVVVVEIVFOLPYNGVTLAQTVIA 289

Qy 286 RLKAVDNTCKLNGSLPVAVITMCEFLGLAHCAMPMLTFAGKXRSRFLSRLTJKUGCTP 345
Db 290 NFNITNSSETSKOLNIAVDVTTSLASVRCVCPNPFYAFIGVKFRSDLFKFLGCLUSQ 349

RESULT 8
A45680
A;Cross-references: UNIPROT:P32248; GB:L08176; NID:9183484; PMID:91833238
A;Reference number: A45680; MUID:93188173; PMID:8383238
A;Status: Preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378

A;Cross-references: UNIPROT:B32248; B-lymphocytes
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIPI:127095)
C;Superfamily: vertebrate rhodopsin

QY 346 ASLCOLCPFPWRSSLSESENATSLTFF 372
 Db 350 ERLRHKWSCHRVNAASVSMELLETTTF 376

RESULT 10

C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: JO1231; A46483

R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Geraz
Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A;Title: Molecular characterization of the interleukin-8 receptor.
 A;Reference number: JO1231; MUID:91378904; PMID:1898400

A;Molecule type: DNA
 A;Residues: 1-355 <RE2>
 A;Cross-references: EMBL:U11870; NID:9511804; PIDN:AAA64378.1; PID:9511805

R;Cross-references: UNIPROT:P21109; GB:M74240; NID:9165438; PIDN:AAA31375.1; PID:9165439
 A;Cross-references: UNIPROT:P21109; GB:M74240; NID:9165438; PIDN:AAA31375.1; PID:9165439

R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992

A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
 A;Reference number: A46483; MUID:92148149; PMID:1737318

A;Accession: A46483; PIDN:AAA31376.1; PID:9165441

A;Cross-references: GB:M82873; NID:9165440; PIDN:AAA31376.1; PID:9165441

A;Experimental source: neutrophils
 A;Note: sequence extracted from NCBI backbone (NCBIN:811526, NCBIPI:811530)

C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.1% ; Score 569; DB 2; Length 355;
 Best Local Similarity 38.3%; Pred. No. 5.6e-42;
 Matches 129; Conservative 52; Mismatches 146; Indels 10; Gaps 7;

QY 7 LEMDLENLEDLF-WELDRLDNYNTDSLIVENHLCPATGCPMLMASFKAVFTPVAVSLLIFLG 65
 Db 1 MEVNWNMTDLWTFEDFANATGMPPVERDYSPLI-VVTOTLNKYYVVIVALVELLS 58

QY 66 VIGNVLVILERHRQTRSSTETFLPHLAVADLLVFLPFAVEAGSISWVLGTFPLCKRV 125
 Db 59 LLGNSLVMVLYLSRSNSRSNTDVYLLNAMADLFLALTPIAVSKKEKGWIFGTFPLCKRV 118

QY 126 IAIKVNFCSSLLIACIAYDRYLAIIVHAYHRRRLSIHTCTGTWLVGFELLALPEI 185
 Db 119 SLRKEVNFVSGILLIACIAYDRYLAIIVHATRTRLTKQRHII-VKFICLGIVWALSLLSLEPF 177

QY 186 LPAKVSGHHNNSLPRCTFSOENQAETHAM-FTSRFLYHVAGFELLPMUYMGWCYVGVTHR 244
 Db 178 LFQYQFS--PNNSSPVC--YEDLGHNTAKMRVYLRLPTFTGFLPLVMLFCYGFTRT 233

QY 245 LRQQRORPQKAVRVALVTSIPLCMSPYHVIFLDTLARKAVDNTCKLNGSLPVAI 304
 Db 234 LFQAA-HMGQKHRANKRVIIFAVVLFCLWMLPYNLVLTADLMRTHVIQETCORNNDIDRL 292

QY 305 TMCCFLGLAHCCANPMLTFAGVFRSDISRLITKLKG 341
 Db 293 DATEILGFLHSCLNPVIIAYFIGQNFRNGFLKMLAARG 329

QY 363 SEN 365
 Db 347 SSN 349

RESULT 11

A39445 Interleukin-8 receptor type A - human
 N;Alternate names: interleukin-8 receptor, high-affinity
 C;Species: Homo sapiens (man)
 C;Accession: 137449; 138710; 138711; A39445

R;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993

A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-8q36 region
 A;Reference number: 137449; MUID:93252387; PMID:84883366

RESULTS 12

A53752 Interleukin-8 receptor (clone 5B1a) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Accession: A53752

R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Naval, J.; Bio. Chem. 269, 12391-12394, 1994

A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A;Reference number: A53752	MUID:94230294; PMID:8175642
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-358 <PRA>	
A;Cross-references: UNIPROT:P35344; GB:L24445; NID:9437661; PID:9437662	
C;Superfamily: vertebrate rhodopsin	
C;Keywords: G protein-coupled receptor; transmembrane protein	
Query Match 28 0%; Score 547; DB 2; Length 358;	
Best Local Similarity 37.2%; Pred. No. 4.7e-40;	
Matches 137; Conservative 50; Mismatches 163; Indels 18; Gaps 9;	
Qy 8 EMDLEN-LEDLFWELDRLDNND-TSIVENHLCPATEGPLMASFKAVFVPVAYSLIPL 63	RESULT 14
Db 3 EFTWENSYEDFFGDFNSYNSYSTDLDPPLTSDAPERSES ---LETNSYTVLVLTVLFL 58	A45747
Qy 64 LGVIGRNVLVILERHRQTRSTSFLEFHIAVDLVLVFLPFAVAEGSVGWLVGTPLCK 123	neuropeptide Y peptide YY receptor Y3 - human
Db 59 LSLLGNSLVMVLVLYSRSCTSVDLYNLAIDLFLATTLPINASASKVHGWTVGTPLCK 118	N;Alternative names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; C;Species: Homo sapiens (man)
Qy 124 TVIALHKVNPFYCSSLACIAYDRLAIVAHAYRHRRLSITHTCTGTTIWYGFLLALP 183	C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: A45747; A53103; I53006; I59444; I69203; S32761
Db 119 VVSILVERVNFYSGILLACIAYDRLAIVAHAYRHRRLSITHTCTGTTIWYGFLLALP 177	R;Federer, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Liu, Genomics 16, 707-712, 1993.
Qy 184 EILFAKUSQGHANNSLPRLPCTPSQENQAEATHAW-FTISRFLYHAGELLPMVGMGCVYGVV 242	A;Title: Molecular cloning of a human seven-transmembrane domain receptor, LESTR, that is highly similar to the bovine neurokinin-1 receptor. A;Reference number: A45747; MUID:94103215; PMID:8325644
Db 178 ILLFENAI-I-FFPNSSPVCFYEDMGN - STAKWRYVLRILLPQTFGTLPILVLMFCYVFL 233	A;Accession: A45747; A;Molecule type: mRNA A;Residues: 1-352 <FED>
Qy 243 HRLRQORPRQRKAVRVALVTSIFLCLSPYHVIVIFLDTLARLKAIVDTCKLNGSLPV 302	A;Cross references: UNIPROT:P61073; PIDN:9292516; PID:AAA16617-1; PID:929292:
Db 234 RTLFOA-HMGOKHRAMRVIFAVVFLCPLPNLVLTDTMLMRTHVQETCBRRNDIR 292	R;Loetscher, M.; Geibar, T.; Zwahlen, R.; Baggioolini, M.; Moser, B.
Qy 303 AITMCEFLGLAHCCINPMLTFAGYKFRPSLDSRLTFLGTCPLCQPSLCSRSSUSE 362	J. Biol. Chem. 269, 232-237, 1994
Db 293 ALDATEILGFLHSCLNPPIYAFIGOKFRYGLLKTLAAHGLJSKEFLAK--ESRPSFVAS 349	A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly similar to the bovine neurokinin-1 receptor. A;Reference number: A53103; MUID:94103215; PMID:827679
Qy 363 SENATSLT 370	A;Accession: A53103; A;Molecule type: mRNA A;Residues: 1-352 <LOE>
Db 350 SSGNTST 357	A;Cross references: ENBL:X71635; PID:9297099; PIDN:CAA50641-1; PID:9297100 R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
RESULT 13	R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Int. Immunol. 5, 1239-1249, 1993
G00048 fusin (LESTR) - crab-eating macaque	A;Title: Molecular cloning, characterization, and localization of the human homolog to the bovine neurokinin-1 receptor. A;Reference number: I53006; MUID:93319629; PMID:8329116
A;Species: Macaca fascicularis (crab-eating macaque)	A;Accession: I53006; A;Molecule type: mRNA A;Residues: 1-352 <HER>
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004	A;Cross references: GB:L06797; PID:914922; PIDN:AAA03205-1; PID:914928
C;Accession: G00048	R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
R;Natsumi, M.	Regul. Pept. 47, 247-258, 1993
Submitted to GenBank, July 1996	A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolog. A;Reference number: I59444; MUID:94052833; PMID:8231909
A;Reference number: H00048	A;Accession: I59444; A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Accession: G00048	A;Molecule type: mRNA A;Residues: 1-352 <RB2>
A;Species: Macaca fascicularis (crab-eating macaque)	A;Cross references: GB:L01639; PID:9189313; PIDN:AAA16594-1; PID:9189314
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004	R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
A;Cross-references: UNIPROT:Q28474; GB:D86579; NID:91468948; PID:91468949	Int. Immunol. 5, 1239-1249, 1993
C;Superfamily: vertebrate rhodopsin	A;Title: Molecular cloning of cDNAs encoding a LDP78 receptor and putative leukocyte chemoattractant receptor-2.
Query Match 27.8%; Score 543; DB 2; Length 352;	A;Reference number: I54751; MUID:94092629; PMID:7505609
Best Local Similarity 34.2%; Pred. No. 1e-39;	A;Accession: I69203; A;Molecule type: mRNA A;Residues: 1-352 <RES>
Matches 113; Conservative 69; Mismatches 124; Indels 24; Gaps 4;	A;Cross references: GB:D10924; PID:9219868; PIDN:BA01722-1; PID:9219869
Qy 47 ASFKAVFVAYSLIFLGLVYIPLIYIPLTFLCKTVIALHKVNPFYCSSLACIAYDRLAIVHAYRHRRLSI 166	C;Genetics: A;Gene: GDB:NPY3B; NPY3 A;Cross references: GDB:NPY3B; NPY3
Db 34 AHFNRIFLPIYIPLTFLCKTVIALHKVNPFYCSSLACIAYDRLAIVHAYRHRRLSI 166	A;Cross references: GDB:230002; OMIM:162643
Qy 107 AVAEGSVNWLGVTFPLCKTVIALHKVNPFYCSSLACIAYDRLAIVHAYRHRRLSI 166	A;Map position: 2q21-2q21
Db 94 WADDAVANNFGNFLKAVHVTYTNLYSSVNLFIISLRLAIVHATNSQPRKLIA 153	C;Superfamily: vertebrate rhodopsin
Qy 167 HITCGTIWYGFLLALPEILPAKYSQ-----HHNSLSPRCTFSQENQAETHAWRTS 218	C;Keywords: G protein-coupled receptor; transmembrane protein
Db 154 KVYVGWVWIPALLTIPDFIFASVSEADDYICCDRFYNDLWWVF----- 199	Query Match 27.6%; Score 540; DB 2; Length 352; Best Local Similarity 33.9%; Pred. No. 1.e-39;

Matches 112; Conservative 70; Mismatches 124; Indels 24; Gaps 4; Search completed: August 29, 2005, 23:57:44
 Job time : 42 secs

QY 47 ASFKAVFPVAYSLIFLVLGVIGNVLYVILERHROTSSTETPLFLAVADLLVFILEP 106
 Db 34 ANFENKLFPLPTYSIPLPLTGVNGNLVILVNGYQKRLRSMTDKYRLHLSYADLILPFVITLPP 93

QY 107 AVAEGSGVWLGTPLCFTVIALHKVNYFCSSLLACIATVLAIRVHAYRERRLSI 166
 Db 94 WADVAVANNYFGNFLCKAVHVITYNLYSSVLLAFISLDRYLAIVATNSQRERKLAE 153

QY 167 HITCGTFLWLGFLLAPEILPAKVSGG-----HHNNSLPRTCFSQENQAETHAWFTS 218
 Db 154 KVVYGVWIPALPLTIPDFIFANVSEADDYICDRFYPNPLWWVVF----- 199

QY 219 RFLYHVGAFPLPMLVNGWCYVGVVHRLRQDQRQPQRQAVRVALVTSPFLCNSPHTIV 278
 Db 200 QFOQHMVGILTPLGPVITLSCYCILISKLSSKGH-QKRAALKTFTVILLIAFFACUPLVYTG 258

QY 279 IFLDPTLARLKAVDNTCKLNGSLSPVLTMCPLGLAHCAINPMLYTAGVYKFRSDLSRLLT 338
 Db 259 ISIDSFILLEIKQGCEPENTVHMKISTEALAFFHCUNPILYAGFAKEFKTSQAHLT 318

QY 339 KLGGCTGPASLSQLFPSSWRSSLS-ESENAT 367
 Db 319 SVSRGSSLKTLSKGRKGHSVSTESSESSS 348

RESULT 15
 S28787
 neuropeptide Y/neuropeptide YY receptor Y3 - bovine
 C;Species: Bos primigenius taurus (cattle)
 e;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: S28787
 R;Rimland, J.; Xin, W.; Sweeney, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
 Mol Pharmacol. 40, 869-875, 1991
 A;Title: Sequence and expression of a neuropeptide Y receptor CDNA.
 A;Reference number: S28787; MUID:92100053; PMID:1661837
 A;Accession: S28787
 A;Molecule type: mRNA
 A;Residues: 1-353 <RIM>
 A;Cross-references: UNIPROT:P25930; EMBL:M86739
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 537.5%; DB 2; Length 353;
 Best Local Similarity 33.6%; Pred. No. 3.1e-39;
 Matches 118; Conservative 69; Mismatches 145; Indels 19; Gaps 6;

QY 25 DNYYNDTSLVENHL----CPATEGPMASFKAVFVPLGTVTSLIPFLGTVTGNVTLVIER 78
 Db 10 DNYYTEDLSSGDDYSMSMKEPFPREEN--AHENRFLPLTVTSLIPFLGTVNGLVLYNGY 66

QY 79 HROTRSTSSTELFLHLAVADLLVFLPLPFAVAEGSVWVLTGFLCKTVIALHKVNFYCSSL 138
 Db 67 QKQLRSMTDKYRLHLSVADLFLVITLPLPWAVIDAANWEGKFPLCKAVVITYTNLYSSVL 126

QY 139 LLACTAVDRLAIVAHVAYRHRLLSIIHITCGTIVLWLGFLLAPEIPAKYQSQHANS 198
 Db 127 ILAFISLDRYLAIVATNSOKPRKLLAEKVVYGVWLPAVLTPIDLIFADIEKVDERYI 186

QY 199 LPRCTFSQENQAETHAWF-TSRFLYHVAEPLPMLVMGCVYVHRLRQAQRPRORKA 257
 Db 187 CDRFVPSD-----LWLVVFQFOHIVVGLLPGIVIVCYCLISCYLKSLSH-KGYQKREKA 238

QY 258 VRVAILVTSIPLCNSPHTIVFLDTLARLKAVDNTCKLNGSLPVATMCFLGLAHCCL 317
 Db 239 LKTTVILILTFACOLPYTIGISIDSFILELIIOQCEPESTVHKWISITEAFLFHCCCL 298

QY 318 NPMLYTAGVYKFRSDLSRLTKLGTPASLCOLEPSPWSRSSLS-ESENAT 367
 Db 299 NPILYAFLGAKFKTSQAHLTSVSRGSLSKILSKGRKGHSVSTESSSSS 349

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Scoring table:	BLOSUM62				
Searched:	1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0‡ Maximum Match 100‡ Listing first 45 summaries				
Database :	UniProt_03: 1: uniprot_sprot:*				
	2: uniprot_trembl:*				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Match	Length	DB ID	Description
1	1953	100.0	372	1 CCR5_HUMAN	P32302 homo sapien
2	1658	83.9	374	2 Q6P3C2	Q653C2 mus musculu
3	1615	83.7	374	1 CCR5_MOUSE	Q6d683 mus musculu
4	1590	81.4	374	1 CCR5_RAT	P34997 rattus norv
5	866.5	44.4	392	2 Q932E1	Q93281 Gallus gallu
6	646	33.1	366	2 Q867B2	Q87fb2 capra hircu
7	638.5	32.7	390	2 Q6GNB2	Q6gnne2 xenopus lae
8	635	32.5	368	1 CCR3_HUMAN	P45682 homo sapien
9	635	32.5	415	2 Q7ZTJ0	Q7ZTJ0 homo sapien
10	615	31.5	367	2 Q9QW6	Q9Qw66 mus musculu
11	614	31.4	367	1 CCR3_MOUSE	Q86410 mus musculu
12	613	31.4	367	2 Q9JL19	Q9jli9 rattus norv
13	607	31.1	374	2 Q8O2H1	Q8O2H1 petromyzon
14	606	31.0	355	2 Q8HZN4	Q8hzn4 percopithac
15	601.5	30.8	355	2 Q8HZN8	Q8hzn8 pan troglod
16	594.5	30.8	360	1 IL8B_HUMAN	P2025 homo sapien
17	599.5	30.7	355	1 Q8HZN5	Q8hzn5 macaca mula
18	596.5	30.5	355	2 Q8HZN7	Q8hzn7 gorilla gor
19	595	30.5	378	2 CKR7_HUMAN	P32248 homo sapien
20	595	30.5	378	2 Q8HZF6	Q8hzr6 macaca mula
21	594.5	30.4	353	1 IL8B_PANTR	Q8807 pan troglod
22	590.5	30.2	355	2 Q8HZN3	Q8hzn3 papio hamad
23	585.5	30.0	353	1 IL8B_GORGO	Q28422 gorilla gor
24	579.5	29.7	353	1 IL8B_MACMU	Q28519 macaca mula
25	577.5	29.6	352	2 Q810T4	Q810t4 cavia porce
26	576.5	29.5	378	2 Q8CA82	Q8ca82 mus musculu
27	576	29.5	380	2 Q86LS1	Q86181 sus scrofa
28	575	29.4	378	2 Q6UD6	Q6ud2d6 rattus norv
29	571.5	29.3	378	1 CKR7_MOUSE	P47774 mus musculu
30	569	29.1	355	1 IL8A_RABBIT	P21109 oryctolagus cuniculus
31	568.5	29.1	355	2 Q8HZN6	Q8hzn6 pongo pygma

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Db	241	VYHLRLQRQRQPKAIVRVALVTSIFFLCWSPHIVFIDTLARLKAVDNTCKLNGSL	300
Qy	301	PVAITMCEFGLAHCLNPMLYTFAGKERSDSLSSLLTKUGCTGPAASLCQLFFPSWRSLL	360
Db	301	PVAITMCEFGLAHCLNPMLYTFAGKERSDSLSSLLTKUGCTGPAASLCQLFFPSWRSLL	360
Qy	361	SSEBNATSLLTF	372
Db	361	SSEBNATSLLTF	372

1	MNYPLTLEND--LENLEDLFWELDRLNDNTDSLIVENHLLCPATEGSPMASFKAVEPVYAY	58
1	MNYPLTLDMGSITYNMDDLYKELAFYSNSTEPIQDSNFCSTVEGPLTSLSPKAVEMPYAY	60
59	SIFLFLGVGNVLVILVILERHRHQTSSTEFLFHIAVADLILVPLPFAVAEGSGVWGLG	118
61	SIFLFLGMGNILVILVILERHRHQTSSTEFLFHIAVADLILVPLPFAVAEGSGVWGLG	120
119	TFLCKTVIALHKVNFCSSILLACIADVRYLAIVAHAYRHRRLSIIHTCGPTWLVGF	178
121	TFLCKTVIALHKVNFCSSILLACIADVRYLAIVAHAYRHRRLSIIHTCTAWLGF	180
179	LALPELIPAKVSQGHANNSLPRTCSQENQAETHAWFTSRFLTHVAGELLPLVMGNCY	238
181	LFLAPELIPAKVGQPNNDSLPOCTSQEAEATRAWFTSRFLYHGGEPLVMGNCY	240
239	VGVVHLRLQARQRQRQKAVRVALVTSIFFLCLMSPYHIVFIDLTALARUKAVDTICKLG	298
241	VGVVHLRLQARQRQRQKAVRVALVTSIFFLCLMSPYHIVFIDLTALARUKAVNSSCELSG	300
299	SIPVATITMCBFLGLAHCCLNPMLYTFAGYKFRSDLSRLRTKLGTGPASLCOLFPWSRRS	358
301	YLSVATITCFLGLAHCCLNPMLYTFAGYKFRSDLSRLRTKLGAAPSLCOLFPNWRKS	360
359	SLSSESENATSLITTF	372
361	SLSSESENATSLATTE	374

SULT 3	R5_MOUSE	STANDARD;	PRT;	374 AA.
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	004683;	(Rel. 27, Created)		
	01-OCT-1993	(Rel. 27, Last sequence update)		
	01-OCT-1993	(Rel. 45, Last annotation update)		
	25-OCT-2004	(Rel. 45, Last annotation update)		
	C-X-C chemokine receptor type 5 (CXC-R5) (CXCR5)	receptor 1 homolog).		
	Name=Bar1; Synonyms=Cxcr5, Gpcr6;			
	Mus musculus (Mouse).			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Mu-			
	NCBI_TaxID=10090;			
	[1]			
	SEQUENCE FROM N.A.			
	STRAIN=BALB/C; TISSUE=Liver;			
	STRAIN=BALB/C; TISSUE=Liver;			
	MEDLINE=94090211; PubMed=8405054;			
	Kaiser B., Poerster R., Wolf I.I., Epensperger C.			
	"The G protein-coupled receptor B1R is involved in differentiation and is also expressed in neuro-			
	PR-1 ImmunoC 22:253-253 (1993)			

[2] SEQUENCE OF 151-269 FROM N.A.
TISSUE-TESTIS; MEDLINE=9116980; PubMed=8388218;

Willkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I., Copeland N.G., Jenkins N.A.; "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors." ; Genomics 18:175-184 (1993). [3]

CHARACTERIZATION MEDLINE=97133211; PubMed=8378608; DOI=10.1016/S0092-8674(00)81798-5

Foerster R., Matsumoto A.E., Kremmer E., Wolf E., Brem G., Lipp M.; "A puractive chemokine receptor, BLR1, directs B cell migration to spleen." ; Cell 87:1037-1047 (1996). [4]

LIGAND BINDING. MEDLINE=98146056; PubMed=9386651; DOI=10.1038/35876; Williams M.D., Ng V.N., Ansel K.M., Ekland E.H., Cyster J.G., Williams L.T.;

RT	"A B-cell-homing chemokine made in lymphoid follicles activates Burkitt's lymphoma receptor-1."	
RT	Nature 391:798-803(1998).	
RL	- - FUNCTION: Cytokine receptor that binds to B lymphocyte chemoattractant (BLC). Involved in B-cell migration into B-cell follicles of spleen and Peyer's patches, but not in those of mesenteric or peripheral lymph nodes.	
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.	
CC	- - TISSUE SPECIFICITY: Mainly in spleen, in resting B-cells.	
CC	- - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	EMBL; X71788; CAA0673_1; -;	
DR	EMBL; I20332; AAA6885_1; -;	
DR	PIR; S42628; S42628.	
DR	MGD; MGI:103567; Blrl1.	
DR	InterPro; IPR000248; Angpt2_receptor.	
DR	InterPro; IPR001055; CXCR5_Receptor.	
DR	InterPro; IPR000276; GPCR_Rhodopsin.	
DR	Pfam; PF00001; 7tm_1..1.	
DR	PRINTS; PR00241; ANGIOGENINSIR.	
DR	PRINTS; PR00564; CXCCMKKINERS.	
DR	PRINTS; PR00327; GPCRHHDDOPEN.	
DR	PROSITE; PS00037; G-PROTEIN_RECCEP_F1_1..1.	
DR	PROSITE; PS50262; G-PROTEIN_RECCEP_F1_2..1.	
B-KW	B-cell activation; G-protein coupled-receptor; Glycoprotein; Transmembrane.	
KW	DOMAIN; 1..57	Extracellular (Potential).
FT	TRANSMEM..58	1 (Potential).
FT	TRANSMEM..78	Cytoplasmic (Potential).
FT	TRANSMEM..90	2 (Potential).
FT	TRANSMEM..111	Extracellular (Potential).
FT	TRANSMEM..126	3 (Potential).
FT	TRANSMEM..147	Cytoplasmic (Potential).
FT	TRANSMEM..148	4 (Potential).
FT	TRANSMEM..169	Extracellular (Potential).
FT	TRANSMEM..170	5 (Potential).
FT	TRANSMEM..190	Cytoplasmic (Potential).
FT	TRANSMEM..221	6 (Potential).
FT	TRANSMEM..242	Extracellular (Potential).
FT	TRANSMEM..243	7 (Potential).
FT	TRANSMEM..261	Cytoplasmic (Potential).
FT	TRANSMEM..262	N-linked (GlcNAc. . .) (Potential).
FT	TRANSMEM..283	N-linked (GlcNAc. . .) (Potential).
FT	TRANSMEM..306	Potential.
FT	TRANSMEM..307	385258420C1EDE30 CRC64;
FT	TRANSMEM..327	
FT	TRANSMEM..374	
FT	TRANSMEM..328	
FT	CARBOHYD..28	
FT	CARBOHYD..28	
FT	CARBOHYD..198	
FT	DISTOFID..124	
SQ	SEQUENCE..374 AA: 42:00 MW: 83.74 % Score: 1635; DB 1; Length: 374;	
	Query Match Best Local Similarity 83.74%; Pred. No. 7..1e-10; Mismatches 29; Conservative Matches 310; Indels 2; Gaps 1;	
Qy	1 MNYPATLEMD..LENLEDLFWELDLRDLNDNTSLVNEHICPATGSPLMASFKAVEPVAY 58	
Db	1 MNYPATLDGSITVNMDDIKEFLAFYNSSTEIPQDSNCSTVGPLLSITFCPKAFMPVAY 60	
Qy	59 SLIFLPGIGNVLYVILVERHRQTRSSTETFLPLAVADLLVPTLPFAVAEGSVWVLG 118	
Db	61 SLIFLGMGNVLYVILVERHRHTRSTSSTFLPLAVADLLVPTLPFAVAEGSVWVLG 120	
Qy	119 TFLCKTVIAHLKINFYCSILLACIADVRLAIYHAYHAYRHLISIHTCGTIVLG 178	
Db	121 TFLCKTVIAHLKINFYCSILLACIADVRLAIYHAYHAYRRLISIHTCTAILWAGP 180	
Qy	181 LFALPELLPAVKGPHANNLSPQTSQNEAEIRAWFSTRLFLYIGGFLPLYMGHGY 240	

Qy	239	VGVVHLRQORRPOKAVRVALIVTSPPLCNSPYHIVIFDLTALARIKAVDNTCKLNG	298		PT	TRANSMEM	222	242	5 (Potential).
Db	241	VGVVHLRQLQQRRPOKAVRVALIVTSPPLCNSPYHIVIFDLTALARIKAVNNSCELSG	300		PT	DONAIN	243	262	6 (Potential).
DT	01-FEB-1994	(Rel. 28; Created)			PT	TRANSMEM	262	282	Extracellular (Potential).
DT	01-FEB-1994	(Rel. 28; Last sequence update)			PT	TRANSMEM	283	305	
DT	25-OCT-2004	(Rel. 45; Last annotation update)			PT	DONAIN	307	327	7 (Potential).
DE	C-X-C chemokine receptor type 5 (CXCR-5) (Burkitt's lymphoma receptor 1 homolog) (Neurolymphatic receptor) (NLR).				PT	CARBOHYD	328	374	Cytoplasmic (Potential).
GN	Name=Bir1; Synonyms=Cxcr5;				PT	CARBOHYD	28	28	N-linked (GlcNAc. .) (Potential).
OS	Rattus norvegicus (Rat).				PT	CARBOHYD	198	198	N-linked (GlcNAc. .) (Potential).
OC	Mammalia; Eutheria; Rodentia; Chordata; Vertebrata; Buteleostomi; Muridae; Murinae; Rattus.				PT	DISULFID	124	204	Potential.
OX	[1]				PT	DISULFID	124	204	
RP	SEQUENCE FROM N.A.				SQ	SEQUENCE	374 AA:	42012 MW:	D87A2AC816207319 CRC84;
RC	SEQUENCE=Spleen; MEDLINE=P3238948; PubMed=8386678; DOI=10.1016/0014-5793(93)80102-Z; RA	Kouba M., Vanetti M., Wang X., Schaefer M., Hoeltl V.; RT	"Cloning of a novel putative G-protein-coupled receptor (NLR) which is expressed in neuronal and lymphatic tissue."; RL	PEBS Lett. 322:173-178 (1993).	Query Match	81.4%; Score 1590; DB 1;	Length 374;		
CC	-1- FUNCTION: Cytokine receptor that binds to B lymphocyte chemotactant (BLC) (By similarity).				Best Local Similarity	81.0%; Pred. No. 8.4e-101;			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				Matches	303; Conservative 27; Mismatches 42; Indels 2; Gaps 1;			
CC	-1- TISSUE-SPECIFICITY: Expressed in neuronal and lymphatic tissue.								
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				RESULT	5			
DR	PIR: S71463; CAAS0582.1; -.				ID	093281	PRELIMINARY;	PRT:	392 AA.
DR	PRINTS: PR0054; CXCCMKINNSR.				AC	093281;			
DR	PRINTS: PR00237; GPROTEINRECEP_F1_1; -.				DT	01-NOV-1998	(TRMBLrel. 08; Created)		
DR	PROSITE: PS00237; G PROTEIN RECEPTOR.				DT	01-NOV-1998	(TRMBLrel. 08; Last sequence update)		
DR	InterPro: IPR001053; CXC_5_Receptor.				DT	01-JUN-2003	(TRMBLrel. 24; Last annotation update)		
DR	InterPro: IPR002276; GPCR_Rhodopsin.				DE				
DR	Pfam: PF00001; 7tm_1; 1.				GN	Name=CRBL1;			
DR	PRINTS: PR00241; ANGIOTENSIN_INR.				OS	Gallus gallus (Chicken)			
DR	PRINTS: PR0054; CXCCMKINNSR.				OC	Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
DR	InterPro: IPR00248; Angtn2_receptor.				OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
DR	InterPro: IPR001053; CXC_5_Receptor.				OC	Archosauuria; Aves; Neognathae; Galliformes.			
DR	InterPro: IPR000276; G-protein coupled receptor.				OX	Gallus.			
DR	PROSITE: PS50062; G-protein coupled receptor.				RN	[1]	SEQUENCE FROM N.A.		
DR	kw B-cell activation, G-protein coupled receptor; Glycoprotein; Transmembrane.				RX	MEDLINE=98244380; PubMed=9584981;			
kw	DOMAIN 1 57				RA	Gupta S.K., Pillarisetti K., Gray S.L., Stadel J.M.; Stadel J.M.; Molecular cloning of a novel chemokine receptor-like gene from early stage chick embryo.,			
FT	TRANSMEM 58 78				RT	Biogchem. Mol. Biol. Int. 44:673-681(1998).			
FT	TRANSMEM 79 90				RL	DR BMBL; AF02939; AAC2395.1/-.			
FT	TRANSMEM 91 111				DR	GO; GO:0016021; C:integer to membrane; IEA.			
FT	TRANSMEM 112 126				DR	GO; GO:0016493; F:C-C Chemokine receptor activity; IEA.			
FT	TRANSMEM 127 147				DR	GO; GO:0016494; F:C-X-C Chemokine receptor activity; IEA.			
FT	TRANSMEM 148 169				DR	GO; GO:00014872; F:receptor activity; IEA.			
FT	TRANSMEM 170 190				DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.			
FT	TRANSMEM 191 221				DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.			
FT					DR	InterPro; IPR000355; Chmkine_Receptor.			

DR	InterPro; IPR001053; CXC_5_receptor.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PRO0057; CCCHMOKNER.			
DR	PRINTS; PRO1532; CXCHMOKNER3.			
DR	PRINTS; PRO0237; GPCRHRDOPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1;			
DR	PROSITE; PS00262; G-PROTEIN_RECEP_F1_2;			
KW	G-protein coupled receptor; RecepFor; Transmembrane.			
Receptor				
SEQUENCE	392 AA; 44760 MW; 3B5CFC88366F088 CRC64;			
Query Match	44.4%; Score 866.5; DB 2; Length 392;			
Best Local Similarity	48.4%; Pred. No. 2.1e-51;			
Matches	169; Conservative 57; Mismatches 116; Indels 7; Gaps 3;			
Qy	28 NDTSLVHENLCPATEGPMAS---EKAIVFVPAVAYSLIPLGVIGNVILVILERHROTR 83			
Db	47 NTTPSLEGYFCNPSSLWLANQDPRKVFIPPLAYLMLFVQLGTQVNQNALVTLERPSR 106			
Qy	84 SSTETFLFLAVDLLNFIPLPAVAEESVGWLGTFLCKTVIALHKVNFYCSLLIACI 143			
Db	107 TTENFLFLTANLALLTFPSVSVESLAGWVFGTFLCKLISAVHKNFYHEAAGLH 166			
Qy	144 AVDRYLAIVHAHVAYHARLSSLTHITCTGTVLGFLLALPEILFAKVYSQGHNNSLPRT 203			
Db	167 RVDYLAIVATHYRKARARSILHTCAIWLSLTLTLPDLFMEWTDESNRSL-CY 224			
Qy	204 FSENQAASTHAWTSRSRFYHVAGFLLPMLVMGCVYGVVHLRQAQRPOROKAVRAIL 263			
Db	225 FPEAGIHNWNVLATREFLYHSVCFEMPILVCMYCALVRLTCQSRL-QRQAKAVRAIL 283			
Qy	264 VTSIFFLSPWSPHIVIFDFTLARLKAVNTCKLNGSLVEATMCPEFLGAHCCLNPMLYT 323			
Db	284 VIGVFLCWSPHIVIFVINTLKEAFKDCLLEDHTAINVTEAIGFTHCCLNPIYA 343			
Qy	324 FAGVKFRSDLSRLITLTKCTGPASLCLQFPSSWRSSLSSESENATSLTTF 372			
Db	344 FIGVKFRDFRITLHELGSCISQETLQEILEVTRKGCGIESDNTTSISTF 392			
RESULT 6				
Q867B2	PRELIMINARY; PRT; 366 AA.			
ID	Q867B2	PRELIMINARY;	PRT;	366 AA.
AC	Q867B2;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)	Created		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	CXC chemokine receptor 3.			
GN	Name=cxcr3;			
OS	Capraria hircus (Goat).			
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Capra.			
OC	Caprinae; Capra.			
NCBI_TaxID	9925; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
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RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
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RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
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AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
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RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
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RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
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RP	SEQUENCE FROM N.A.			
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TISSUE	Spleen;			
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AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [1]			
RN				
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
TISSUE	Spleen;			
ID	Q6GNE2	PRELIMINARY;	PRT;	390 AA.
AC	Q6GNE2;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	LOC436699 protein (Fragment).			
GN	Name=LOC436699;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.			
OC	Xenopoda; Xenopus.			
NCBI_TaxID	8355; [

Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).

SEQUENCE FROM N.A.
TISSUE=Spine;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Straubberg R.L., Wagner L., Pontius J., Clifton S.M.,
Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.," *Dev. Dyn.* 225:384-391 (2002).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Spine;
RA Klein S., Gerhard D.S.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL: BC073571; AA173571.1; -.
DR GO; GO:0016021; C:Integral membrane protein activity; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0001584; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . . : IEA.
DR InterPro; IPR004355; Chmkine receptor.
DR InterPro; IPR004070; CXCR_3 receptor.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR000637; CCHEMKINER.
DR PRINTS; PR01532; CACCHMKINER.
DR PROSITE; PS00237; GP0RHOPOSN.
DR PROSITE; PS00237; G_PR0TEIN_REC0P_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PR0TEIN_REC0P_FL_2; 1.
SQ NON TER 1 390 AA; 44470 MW; 44294 0606DCA920 CRC64;
SEQUENCE : Query Match 32.7%; Score 638.5; DB 2; Length 390;
: Best Local Similarity 39.8%; Pred. No. 7.6e-36;
. Matches 130; Conservative 64; Nsmatches 118; Indels 15; Gabs 5;
: .
QY 49 FKA[VFPVAVASLIFLFLGIVGNLVILVILVERHROTRSTETFLHLADILLYELLPPAV 108
: |||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
QY 67 FDRRLPLPAF5IVFLGMLGNVLVLLQVNRWLIQLSTDIFLHLADILLYLLTPWA 126
DB 109 AEGSYGVWLGFLKTVIYAHKVNPFYCSILLATACDVYLAITAHVAYHRRLLSI 168
: .
QY 127 TQAVSGWIFENVLCKRMVASIFKINFYACTFLVCLTSQRDYLSTIVAVQLYKHHRLVHW 186
DB 169 TCGTIIWLGVGFPLALPEILFAKVSQGHNNSLPRCTFS---QENQAEHTAWFST-RFYH 223
QY 187 SCLLWCLCGLSIPPMVYTRVYE----PRANVTDQOPDFGHLDSTKWTKLSTFLYH 240
DB 224 VAGFLPLMVGWCYVGVHRLRQAQRPRQKAVRAVLTSTIFFLWSPHIVIFLDT 283
: |||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
QY 241 IVGFLPLCPMVYCYTHISLSCQTHF-EKQKALRVIAVVVFFLCTPNIVALLDT 299
DB 284 LARLKAVDNTCKLNSSLPVAITMCBFLGLHCUNPMLTFAGYKFRSDLSRLTLCCT 343
QY 300 MNILAVLPDNCTTDSNIDIALSVTSGLCYFHSCLNPLYYAFVGAKPKMVKLVELINKSLCI 359
DB 344 GPASILCQLF---PSWRRSSLSSESENAT 367
QY 360 CPQIVKXKIKNPPAKPTWSESGDTT 386
DB RESULT 8
ID CCR3_HUMAN STANDARD; PRT; 368 AA.
AC P49828; O15185; Q9P2T4; Q9P2T5;
DT 01-OCT-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXC-R3) (CCR-L2) (CD183

DE antigen).
NAME=CXCR3; Synonyms=GPR9;
Homo sapiens (Human).
OS Homo sapiens
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L., Clark-Lewis I., Baggioini M., Moser B.; "Chemokine receptor specific for IP10 and mig: structure, function, and expression in activated T-lymphocytes."; *J. Exp. Med.* 184:963-969 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Guierrez J., Varona R., Zaballos A., Lind P., Marquez G.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Warren C.N., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cDNA.org)." ; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Testis;
RA MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.R., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettenbach M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmidt J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 5-368 FROM N.A.
RX MEDLINE=96115583; PubMed=8666360;
RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R., Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R., O'Dowd B.F., Docherty J.M.; "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neuropeptide RT and somatostatin receptors.";
RT Genomics 29:335-344 (1995).
RN [6]
RP LIGAND BINDING.
RC TISSUE=Fetal astrocytes;
RX MEDLINE=21040285; PubMed=11196595; DOI=10.1038/sj.j.gene.6363682;
RA Kato H., Tauchiya N., Tokunaga K.; "Single nucleotide polymorphisms in the coding regions of human CXCR3.";
RT Chemokine receptors CXCR1, CXCR2 and CXCR3.;
RN Genes Immun. 1:330-337 (2000).
RN [7]
RP LIGAND BINDING.

"Interferon-inducible T cell alpha chemoattractant (I-TAC): a novel non-ELR CXC chemokine with potent activity on activated T cells through selective high affinity binding to CXCR3."; J. Exp. Med. 187:2009-2021(1998).

-1 - FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC.

-1 - SUBCELLULAR LOCATION: Integral membrane protein.

-1 - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

-1 - DATABASE: NAME=PROW; NOTE=PROW 1:78-83 (2000);
WWW="<http://www.ncbi.nlm.nih.gov/prow/guide/60534941.g.htm>".

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Db	149	YLSIVTHATQIYRRDRRPRVRLTCIVWGLCLFALPDFIYSANTYDORLNA-THCQYNFP	207
Qy	208	NQAETHAWPTSRFLYTHVAGFLPMLVMGWCYVGVVHRLQARPRQRQKAVRVALYTSI	267
Db	208	QVGR-[---ALRVQLQVAGFLPLVMAYCTAHILAVL-LVSRGQRFRAMRLVVVVVA	262
Qy	268	FFELCNSPVHIVIETLTALARVADNTCKLNGSLIPVTAITMCFBLGAHCCLNPMLYTFFGV	327
Db	263	FAVCRTPTVHLVVLQVIMDGVLANCGRSHVDASVTSGMGMHCCLNPLUYAFVGV	322
Qy	328	KPRSDSRLTGTG---GPASLQLPFSMRSSRSSESENATL	369
Db	323	KFREQ@MMALFTRLGRSDORGQPQR--QPSSSRRESSWSETEASYL	365
RESULT 11			
	ccr3_MOUSE	STANDARD;	PRT:
	ID CCR3_MOUSE		367 AA.
	AC 088470		
	DT 16-OCT-2001	(Rel. 40, Created)	
	DT 16-OCT-2001	(Rel. 40, Last sequence update)	
	DT 25-OCT-2004	(Rel. 45, Last annotation update)	
	DE "The CC chemokine receptor type 3 (CXC-R3) .		
	GN Name=Cxcr3; Synonyms=Cnkra3;		
	OS Mus musculus (Mouse).		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	OX NCBI_TaxID=10090;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RX MEDLINE-98316836; PubMed=9653165; DOI=10.1073/pnas.95.14.8205;		
	RA Soto H., Wang W., Strieer R.M., Copeland N.G., Gilbert D.J.,		
	RA Jenkins N.A., Hedrick J., Zlotnick A.;		
	RA "The CC chemokine 6kine binds the CXC chemokine receptor CXCR3." ;		
	RT Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).		
	RC -!- FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC (BY SIMILARITY). Binds to SCYA1.		
	CC -!- SUBCELLULAR LOCATION: Integral membrane protein.		
	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
	CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).		
	CC EMBL; AF045146; AAC40163.1; -.		
	DR MGI; MGI:12772207; Cxcr3.		
	DR InterPro; IPR000355; Chkine receptor.		
	DR InterPro; IPR004070; Cxcr_3_receptor.		
	DR InterPro; IPR000276; GPR_Rhodopsin.		
	DR Pfam; PF00001; 7TM1_1.		
	DR PRINTS; PR01532; CXCCMHKINER2.		
	DR PR000237; GPCRRIODOPSN.		
	DR PROSITE; PS000237; G_PROTEIN_RECEP_F1_1; 1.		
	DR PROSITE; PS50626; G_PROTEIN_RECEP_F1_2; 1.		
	KW G-protein coupled receptor; Glycoprotein; Transmembrane.		
	FT DOMAIN 1 52	Extracellular (Potential).	
	FT DOMAIN 1 53	1 (Potential).	
	FT DOMAIN 1 53	Cyttoplasmic (Potential).	
	FT DOMAIN 1 80	2 (Potential).	
	FT TRANSMEM 89	Extracellular (Potential).	
	FT DOMAIN 1 100	3 (Potential).	
	FT TRANSMEM 125	Cyttoplasmic (Potential).	
	FT DOMAIN 1 147	4 (Potential).	
	FT TRANSMEM 148	Extracellular (Potential).	
	FT DOMAIN 1 189	5 (Potential).	
	FT TRANSMEM 211	Cyttoplasmic (Potential).	
	FT DOMAIN 232	6 (Potential).	
	FT TRANSMEM 233	Extracellular (Potential).	
	FT TRANSMEM 255	7 (Potential).	
	FT DOMAIN 297		
	FT TRANSMEM 320		
	FT DOMAIN 298		

FT DOMAIN	321	367	Cytoplasmic (Potential).
FT DISULFID	123	202	By similarity.
FT CARBOHYD	22	22	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	32	32	N-linked (GlcNAc. . .) (Potential).
SEQ SEQUENCE	41016 MW; 029FB778E3CD4EA CRC64;		
Query Match Score 614; Pred. No. 3 4e-34; Gaps 6; Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;			
Best Local Similarity 31.4%; Query 614; DB 1; Length 367;			
Qy 28 NDTSLVENVHLCPATGPMASFKAYFPVAYSLFLIGVIGNVLVILVERHRQTRSSTE 87	28 NDTSVLENVHLCPATGPMASFKAYFPVAYSLFLIGVIGNVLVILVERHRQTRSSTE 87	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Db 32 NESDFDSPPCPQ--DFSINFDRFLPALYSLFLGLINGAVAAVILSORTALSTD 88	32 NESDFDSPPCPQ--DFSINFDRFLPALYSLFLGLINGAVAAVILSORTALSTD 88	KW G-protein coupled receptor; Receptor; Transmembrane.	
Qy 88 TFLFHLLAVADLVLFLPFVFAVAEGSYGVNLGTFLCKTVALHLKHFNCYCSLLACIAYDR 147	88 TFLFHLLAVADLVLFLPFVFAVAEGSYGVNLGTFLCKTVALHLKHFNCYCSLLACIAYDR 147	SQ Best Local Similarity 38.8%; Score 613; DB 2; Length 367;	
Db 89 TFLFHLLAVADLVLFLPFVFAVAEGSYGVNLGTFLCKTVALHLKHFNCYCSLLACIAYDR 148	89 TFLFHLLAVADLVLFLPFVFAVAEGSYGVNLGTFLCKTVALHLKHFNCYCSLLACIAYDR 148	SQ Best Local Similarity 38.8%; Score 613; DB 2; Length 367;	
Qy 148 YLAIVHAYHAYHRRLLSIHITCGTTINLVGFLLAPELPEAKVSGHINNSLPLCTPSQE 207	148 YLAIVHAYHAYHRRLLSIHITCGTTINLVGFLLAPELPEAKVSGHINNSLPLCTPSQE 207	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Db 208 QVGRT--ALRVQLQVAGFLMLVLYCAYHLAVL-LVSGRQRRAFLVAVLVTSSI 267	208 QVGRT--ALRVQLQVAGFLMLVLYCAYHLAVL-LVSGRQRRAFLVAVLVTSSI 267	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Qy 208 NQAETHAWPTSRFLYVHAGFLPMLVPMGNYCYGVYHRLPQAQRPRPKAVRYAILVTSSI 267	208 NQAETHAWPTSRFLYVHAGFLPMLVPMGNYCYGVYHRLPQAQRPRPKAVRYAILVTSSI 267	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Db 268 PFLCSPYHIVFLDTLARLKAHDNTCKLNGSLPVIAITCEFLGLAHCCLNPMLYTFAGV 327	268 PFLCSPYHIVFLDTLARLKAHDNTCKLNGSLPVIAITCEFLGLAHCCLNPMLYTFAGV 327	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Qy 268 FAVCWTPLVHIVLVDIMDGVLARNCGRKSHDVAKSVTSGNCYMHCCLNPLIYAFGV 322	263 FAVCWTPLVHIVLVDIMDGVLARNCGRKSHDVAKSVTSGNCYMHCCLNPLIYAFGV 322	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Db 328 KFRSDLSRLTLLKGT--GPASILCOLPFWRRSSLSSESENATSL 369	328 KFRSDLSRLTLLKGT--GPASILCOLPFWRRSSLSSESENATSL 369	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Qy 328 KFRSDLSRLTLLKGT--GPASILCOLPFWRRSSLSSESENATSL 365	323 KFRSDLSRLTLLKGT--GPASILCOLPFWRRSSLSSESENATSL 365	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
Db 323 KFRSDLSRLTLLKGT--GPASILCOLPFWRRSSLSSESENATSL 365		DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	
RESULT 13			
Q9JII9 PRELIMINARY; PRT; 367 AA.	0802H1 PRELIMINARY; PRT; 374 AA.		
ID Q9JII9 AC 0802H1	ID Q9JII9 AC 0802H1	RP SEQUENCE FROM N.A.	
DT 01-JUN-2003 (TREMBLrel. 24, Created)	DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)	RP MEDLINE=2255679; PubMed=12671740;	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RA Kuroda N., Umar-Koo T.S., Sato A., Samonte I.E., Figueiroa F.,	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DE Chemokine receptor CXCR4.	RA Mayer W.E., Klein J.;	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	OS Petromyzon marinus (Sea lamprey).	RT Identification of chemokines and a chemokine receptor in cichlid fish shark and lamprey"; Immunogenetics 54:884-895 (2003).	
DE Chemokine receptor CXCR3.	OC Petromyzota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; OC Petromyzontiformes; Petromyzontidae; Petromyzon.	CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	
OS Rattus norvegicus (Rat).	OC Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; OC Muridae; Murinae; Rattus.	CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; OC Petromyzontiformes; Petromyzontidae; Petromyzon.	OX NCBI_TaxID=7757;	DR GO:001786; P:G-protein coupled receptor protein signalin.. . ; IEA.	
RN [1]	RN	DR GO:001786; P:G-protein coupled receptor protein signalin.. . ; IEA.	
RP SEQUENCE FROM N.A. MEDLINE=20285573; PubMed=10825390;	RP SEQUENCE FROM N.A. MEDLINE=2255679; PubMed=12671740;	DR GO:001786; P:G-protein coupled receptor protein signalin.. . ; IEA.	
RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S., RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S., RA "Identification and molecular characterization of rat CXCR3: receptor expression and interferon-inducible protein-10 binding are increased in focal stroke." RTR	RA "Identification and molecular characterization of rat CXCR3: receptor expression and interferon-inducible protein-10 binding are increased in focal stroke." RTR	DR GO:0004945; P:angiotensin type II receptor activity; IEA.	
RR Mol. Pharmacol. 57:1190-1198(2000).	RR Mol. Pharmacol. 57:1190-1198(2000).	DR GO:0016494; P:C-X-C chemokine receptor activity; IEA.	
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	DR GO:0004872; P:receptor activity; IEA.	
CC C: integral to membrane; IEA.	CC C: integral to membrane; IEA.	DR GO:0001584; P:rhodopsin-like receptor activity; IEA.	
DR ENBL: AF2236542; AF076982.1; -.	DR ENBL: AF2236542; AF076982.1; -.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0016021; C:integral to membrane; IEA.	DR GO; GO:0016021; C:integral to membrane; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0016493; P:C-X-C chemokine receptor activity; IEA.	DR GO; GO:0016493; P:C-X-C chemokine receptor activity; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0016494; P:C-X-C chemokine receptor activity; IEA.	DR GO; GO:0016494; P:C-X-C chemokine receptor activity; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0004872; P:receptor activity; IEA.	DR GO; GO:0004872; P:receptor activity; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.	DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.	DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.	DR GO:0001584; P:angiotensin type II receptor activity; IEA.	
DR InterPro; IPR000345; Chkmskin_receptor.	DR InterPro; IPR000345; Chkmskin_receptor.	DR InterPro; IPR000276; GPCR_Rhodpsn.	
DR InterPro; IPR0004070; CX3_3_receptor.	DR InterPro; IPR0004070; CX3_3_receptor.	DR InterPro; IPR000101; 7tm_1; 1.	
DR PrintN; PR00000000; GPCR_Rhodpsn.	DR PrintN; PR00000000; GPCR_Rhodpsn.	DR PrintN; PR00045; CXCHMMKNER4.	
DR PrintN; PR000557; CCCHENOKINER.	DR PrintN; PR000557; CCCHENOKINER.	DR PrintN; PR00237; GPCRHHODPSN.	
DR PrintN; PR01532; CXCHMMKNER3.	DR PrintN; PR01532; CXCHMMKNER3.	DR PrintN; PR00237; GPCRHHODPSN.	
DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.	G-protein coupled receptor; Receptor; Transmembrane.

Db	1	MESDSFED-FWKGEDISNSYSSTLPPFLDAAPCEPESLEINKYFVVIYAWLFLLSLI	59
Qy	68	GNNVLVLERHRQTRSSTETFLFLAVADLLYFILPFAVEGSGVNYLGTEFLCKTYIA	127
Db	60	GNSLMLVILSRGRSVTVDYLNLALADLFLALTPLWAASVNGWFGTFLCKRVSL	119
Qy	128	LHKKNPYCSSLILLACIADYRLAIYHAYHAYHRRLSITHCTIIVGELLALPELFL	187
Db	120	LKEVNFSGTLIACSVDRYLAIVHATRTRLTCRGL-YKFICLISIWGLSLALPVLFL	178
Qy	188	AKVSQGHNSNLPRTCFSONQAEATHAW-FTSRFLYHYAGFELLMLYNGCWVVRHL	246
Db	179	RRTV - YSSNVSPACYEDMN - NTANWRMLLRLLPQSFGFIVVLLMLFCYGTLLTFL	234
Qy	247	QAQRPRQOKAVRVALVTISIPCLCWSPYHIVIFLDTLRKAWDNTCKLNGSLPVAITM	306
Db	235	KA-HNGQKHFMRYVFAVVLFLICWLPTVNLVJLADLMTROVTOETCERNHIDRALDA	293
Qy	307	CFFGLAHCCINPMLYTFAGVKFRSDLSRLTTLKGCTGPASLCCOLPFSWRRSSLSESENA	366
Db	294	TEILGLTHSCUNPLIYAFIQGKFRHGLLKLIAHGLSKDSL---PKDSRSPFGVSSG	349
Qy	367	TSLTT 371	
Db	350	HmSRP 354	

Search completed: August 29, 2005, 23:56:59
Job time : 176 SECs

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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:48:26 ; Search time 42 Seconds
(without alignments)
661.177 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPLTLEMDLENLDLFWE.....PSWRRSSLSESENATSLITP 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cn2_6_ptodata/1/iaa/SA_COMB.pep:
2: /cn2_6_ptodata/1/iaa/5B_COMB.pep:
3: /cn2_6_ptodata/1/iaa/6A_COMB.pep:
4: /cn2_6_ptodata/1/iaa/6B_COMB.pep:
5: /cn2_6_ptodata/1/iaa/PCTUS_COMB.pep:
6: /cn2_6_ptodata/1/iaa/backfile8..pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	372	1 US-08-202-056-5	Sequence 5, Appli
2	1953	100.0	372	1 US-08-076-093A-6	Sequence 6, Appli
3	1953	100.0	372	1 US-08-701-238-6	Sequence 6, Appli
4	1953	100.0	372	2 US-08-284-586-6	Sequence 6, Appli
5	1953	100.0	372	2 US-08-805-478-6	Sequence 6, Appli
6	1953	100.0	372	2 US-08-805-627A-6	Sequence 6, Appli
7	1953	100.0	372	2 US-08-801-238-6	Sequence 6, Appli
8	1953	100.0	372	2 US-08-801-228-6	Sequence 6, Appli
9	1953	100.0	372	3 US-09-104-296-6	Sequence 6, Appli
10	1953	100.0	372	3 US-08-983-493-8	Sequence 8, Appli
11	1953	100.0	372	4 US-09-170-496D-66	Sequence 66, Appli
12	1953	100.0	378	4 US-09-94-016-10255	Sequence 10255, A
13	1947	99.7	372	4 US-09-170-496D-2000	Sequence 200, Appli
14	1635	83.7	374	3 US-08-983-493-6	Sequence 6, Appli
15	635	32.5	368	3 US-08-708-838-2	Sequence 2, Appli
16	635	32.5	368	3 US-08-828-839-2	Sequence 2, Appli
17	635	32.5	368	4 US-09-170-496D-20	Sequence 20, Appli
18	635	32.5	368	4 US-09-620-594-2	Sequence 2, Appli
19	635	32.5	368	4 US-09-607-156-2	Sequence 2, Appli
20	632	32.4	368	4 US-09-170-496D-174	Sequence 174, Appli
21	601.5	30.8	355	1 US-07-756-568-1	Sequence 1, Appli
22	601.5	30.8	355	1 US-08-454-393A-8	Sequence 8, Appli
23	601.5	30.8	355	1 US-08-390-000A-5	Sequence 5, Appli
24	601.5	30.8	355	3 US-08-444-669-8	Sequence 8, Appli
25	601.5	30.8	355	4 US-09-620-573-8	Sequence 8, Appli
26	601.5	30.8	355	5 PCT-US95-00476-8	Sequence 8, Appli
27	601.5	30.8	360	1 US-08-202-056-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-202-056-5
; Sequence 5, Application US/08202056
; Patent No. 544021

GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202, 056
FILING DATE: 25-PEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34, 659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5510
TELEFAX: 415/522-9881
TELEX: 910371-7168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-202-056-5

Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MNYPITLEMDLNLDLFWBDRLNDYNTSLVENHLCPATGPPMASFKAVFPVAYSL 60

Qy

TOPOLOGY: Linear
US - 08 - 076 - 093A - 6

Query Match 100.0% Score 1953; DB 1; Length 372;
Best Local Similarity 10.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MNYPITLEMDLENDFWELDNDNNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
Db 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120
Db 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120

Qy 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180
Db 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180

Qy 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240
Db 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240

Qy 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300
Db 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300

Qy 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360
Db 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360

Qy 361 SESENATSLTF 372
Db 361 SESENATSLTF 372

RESULT 2
US - 08 - 076 - 093A - 6
Sequence 6, Application US/08076093A

GENERAL INFORMATION:
 APPLICANT: Chuntcharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: Jin Kim, K.
 TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34, 659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEX: 415/952-9881

INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 372 amino acids
 TYPE: Amino Acid

TOPOLOGY: Linear
US - 08 - 076 - 093A - 6

Query Match 100.0% Score 1953; DB 1; Length 372;
Best Local Similarity 10.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MNYPITLEMDLENDFWELDNDNNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
Db 1 MNYPITLEMDLENDFWELDNDNNTSLVENHLCPATGPLMASFKAVFVPAVSL 60

Qy 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120
Db 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120

Qy 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180
Db 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180

Qy 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240
Db 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240

Qy 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300
Db 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300

Qy 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360
Db 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360

Qy 361 SESENATSLTF 372
Db 361 SESENATSLTF 372

RESULT 3
US - 08 - 701 - 265 - 6
Sequence 6, Application US/080701265
Patent No. 5776457

GENERAL INFORMATION:
 APPLICANT: Chuncharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: Jin Kim, K.
 TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/076, 093A
 FILING DATE: 11-Jun-1993
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34, 659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEX: 415/952-9881

INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 372 amino acids
 TYPE: Amino Acid

TOPOLOGY: Linear
US - 08 - 076 - 093A - 6

Query Match 100.0% Score 1953; DB 1; Length 372;
Best Local Similarity 10.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MNYPITLEMDLENDFWELDNDNNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
Db 1 MNYPITLEMDLENDFWELDNDNNTSLVENHLCPATGPLMASFKAVFVPAVSL 60

Qy 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120
Db 61 IFLGVIGNVLVILRHRQTRSSTETFLFLAVADLIVFLPFAAEQSGYGVWLCTF 120

Qy 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180
Db 121 LCKVIALHKVNPFCCSLLACIADVRLAIHVAYHRRLISIHTCGT1WLVGTL 180

Qy 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240
Db 181 ALPEILFAKVSQGHINNSLRCTFSQENQAETHAWFTSRFLYHAGFLLPMLYMGCVG 240

Qy 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300
Db 241 VVHLRQAQRPRQAKVARVAILVTSIFFCWSPTHIVFLDTLARLKAVIDNTKLNSL 300

Qy 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360
Db 301 PVATIMCEPFLGLAHCLNPMLYTAGVKFRSDLSRLITKLGCOTPASLQLCPSSWRSSL 360

Qy 361 SESENATSLTF 372
Db 361 SESENATSLTF 372

RESULT 3
US - 08 - 701 - 265 - 6
Sequence 6, Application US/080701265
Patent No. 5776457

GENERAL INFORMATION:
 APPLICANT: Chuncharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: Jin Kim, K.
 TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/076, 093A
 FILING DATE: 11-Jun-1993
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34, 659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEX: 415/952-9881

INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 372 amino acids
 TYPE: Amino Acid

REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-701-265-6

Query Match Score 1953; DB 1; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8.7e-176;
 Matches 372; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 MNYPPLMDEMLENDFWELDLDNYNDTSIVENHLCATEGPLMASKAVFPVAVSL 60
 Db 1 MNYPPLMDEMLENDFWELDLDNYNDTSIVENHLCATEGPLMASKAVFPVAVSL 60
 Qy 61 IFLGVIGNVLVVLIERHQTRSTSSTEFLHLAVADLLVFLPAVAGSTGWLGTTF 120
 Db 61 IFLGVIGNVLVVLIERHQTRSTSSTEFLHLAVADLLVFLPAVAGSTGWLGTTF 120
 Qy 121 LCKTVIALRKVNFCSSILLACIATDVRLAIVAHAYTHRRLISIHTCTGTIWLGRI 180
 Db 121 LCKTVIALRKVNFCSSILLACIATDVRLAIVAHAYTHRRLISIHTCTGTIWLGRI 180
 Qy 181 ALPELFAKYSQGHNNSLPRCTPSQENAEHTAWFTSRFLYAGFLPMLVMGWCYVG 240
 Db 181 ALPELFAKYSQGHNNSLPRCTPSQENAEHTAWFTSRFLYAGFLPMLVMGWCYVG 240
 Qy 241 VVHLRQAQRPQKAVARVAILTSIFPLCWSYYHITFLDTLARLAVDNTCKLNGSL 300
 Db 241 VVHLRQAQRPQKAVARVAILTSIFPLCWSYYHITFLDTLARLAVDNTCKLNGSL 300
 Qy 301 PVAITMCBFLGLAHCCLNPMLYTFAGVKFRSDLRLTKLGCTGPASLICQLPPSWSRSSL 360
 Db 301 PVAITMCBFLGLAHCCLNPMLYTFAGVKFRSDLRLTKLGCTGPASLICQLPPSWSRSSL 360
 Qy 361 SESENATSLTTF 372
 Db 361 SESENATSLTTF 372

RESULT 4
 US-08-284-586-6
 Sequence 6, Application US/08284586
 Patent No. 5840856
 GENERAL INFORMATION:
 APPLICANT: Chuntharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: Jin Kim, K.
 TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/284,586
 FILING DATE:
 CLASSIFICATION: 424

RESULT 5

US-08-805-478-6
 Sequence 6, Application US/08805478
 Patent No. 5844543
 GENERAL INFORMATION:
 APPLICANT: Chuntharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: Jin Kim, K.
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94060
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/805,478
 FILING DATE: 25-Feb-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2P1C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-9881
 TELEX: 910/371-1768
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-805-478-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8.7e-176;
 Matches 372; Conservative 0; Mismatches 0; Gaps 0;
 1 MNYPPLTEMLDENLEDFWELDRDNNDTSLVENHLCPATEGLMASPKAVFVPAVSL 60
 Db 1 MNYPPLTEMLDENLEDFWELDRDNNDTSLVENHLCPATEGLMASPKAVFVPAVSL 60
 Qy 61 IFLLGIVGNVLVVLREHQTRSSTEFHLFLAVADLLVFLPAVAGSGVWLGF 120
 Db 61 IFLLGIVGNVLVVLREHQTRSSTEFHLFLAVADLLVFLPAVAGSGVWLGF 120
 Qy 121 LCKTVIALHKVNFCSSLLIACIAYDRYLAIHVAVHAYHRRLSITHITCGTIWLGFL 180
 Db 121 LCKTVIALHKVNFCSSLLIACIAYDRYLAIHVAVHAYHRRLSITHITCGTIWLGFL 180
 Qy 181 ALPEILFAKYSQGHANNLSPRCTSQENQAEHTAWFTSRFLYAGFLPMLNGWCYVG 240
 Db 181 ALPEILFAKYSQGHANNLSPRCTSQENQAEHTAWFTSRFLYAGFLPMLNGWCYVG 240
 Qy 241 VVHLRQOQRPRQOKARVAILTISIFFLCWSPHIVFLDTLARLKAVDNTCKLNSSL 300
 Db 241 VVHLRQOQRPRQOKARVAILTISIFFLCWSPHIVFLDTLARLKAVDNTCKLNSSL 300
 Qy 301 PVAITMCEFLGLAHCCNPNMLTYFAGVKFRSDLSRLITKLGCTGPASLCOLFPSPWRSSL 360
 Db 301 PVAITMCEFLGLAHCCNPNMLTYFAGVKFRSDLSRLITKLGCTGPASLCOLFPSPWRSSL 360
 Qy 361 SESENATSLTF 372
 Db 361 SESENATSLTF 372

RESULT 6
 US-08-805-627A-6
 Sequence 6, Application US/0802627A
 Pat. No. 5892017
 GENERAL INFORMATION:
 APPLICANT: Lee, James

APPLICANT: Wood, William J.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94060
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winactin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/802,627A
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-802-627A-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8.7e-176;
 Matches 372; Conservative 0; Mismatches 0; Gaps 0,
 1 MNYPPLTEMLDENLEDFWELDRDNNDTSLVENHLCPATEGLMASPKAVFVPAVSL 60
 Db 1 MNYPPLTEMLDENLEDFWELDRDNNDTSLVENHLCPATEGLMASPKAVFVPAVSL 60
 Qy 61 IFLLGIVGNVLVVLREHQTRSSTEFHLFLAVADLLVFLPAVAGSGVWLGF 120
 Db 61 IFLLGIVGNVLVVLREHQTRSSTEFHLFLAVADLLVFLPAVAGSGVWLGF 120
 Qy 121 LCKTVIALHKVNFCSSLLIACIAYDRYLAIHVAVHAYHRRLSITHITCGTIWLGFL 180
 Db 121 LCKTVIALHKVNFCSSLLIACIAYDRYLAIHVAVHAYHRRLSITHITCGTIWLGFL 180
 Qy 181 ALPEILFAKYSQGHANNLSPRCTSQENQAEHTAWFTSRFLYAGFLPMLNGWCYVG 240
 Db 181 ALPEILFAKYSQGHANNLSPRCTSQENQAEHTAWFTSRFLYAGFLPMLNGWCYVG 240
 Qy 241 VVHLRQOQRPRQOKARVAILTISIFFLCWSPHIVFLDTLARLKAVDNTCKLNSSL 300
 Db 241 VVHLRQOQRPRQOKARVAILTISIFFLCWSPHIVFLDTLARLKAVDNTCKLNSSL 300
 Qy 301 PVAITMCEFLGLAHCCNPNMLTYFAGVKFRSDLSRLITKLGCTGPASLCOLFPSPWRSSL 360
 Db 301 PVAITMCEFLGLAHCCNPNMLTYFAGVKFRSDLSRLITKLGCTGPASLCOLFPSPWRSSL 360
 Qy 361 SESENATSLTF 372
 Db 361 SESENATSLTF 372

RESULT 6
 US-08-805-627A-6
 Sequence 6, Application US/0802627A
 Pat. No. 5892017
 GENERAL INFORMATION:
 APPLICANT: Lee, James

RESULT 7
US-08-801-238-6
Sequence 6, Application US/0801238
Patent No. 5919396
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: PFAA RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801.238
FILING DATE: 19-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/552-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-801-238-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYPLTLEMDLENLEDLFWELDRDNNDNTSLVENVHCPATEGPLMASFKAVFPVAYSL 60
Db 1 MYPLTLEMDLENLEDLFWELDRDNNDNTSLVENVHCPATEGPLMASFKAVFPVAYSL 60
Db 1 IFLGVIGVNVLYVILERHRQRTRSSSTEFLFLAVADLLVFLPAVAFEGSGVWLTGTF 120
Db 1 IFLGVIGVNVLYVILERHRQRTRSSSTEFLFLAVADLLVFLPAVAFEGSGVWLTGTF 120
Qy 121 LCKTVIAHKVNFCSSILLACTAVDRYLAIYHVAYRHRRLSTHTCGCTIWGFLI 180
Db 121 LCKTVIAHKVNFCSSILLACTAVDRYLAIYHVAYRHRRLSTHTCGCTIWGFLI 180
Qy 181 ALPEILPAKVSOGHNSLPRCTPSQENQAEATHAWTSFLYVAGFLPMLVMGCVG 240
Db 181 ALPEILPAKVSOGHNSLPRCTPSQENQAEATHAWTSFLYVAGFLPMLVMGCVG 240
Qy 241 VVHLRLQRQRQRQKAVRVALVTSIFFLCMSPHYIVFLDTLARAKVDNTCKLNGSL 300

Db 241 VVHLRLQRQRQRQKAVRVALVTSIFFLCMSPHYIVFLDTLARAKVDNTCKLNGSL 300
Qy 301 PVAITMCEFLGLAHCCNLPMLYTFAGYKFRSDLSRLTLKGCTGPASICQQLPFSWRSSL 360
Db 301 PVAITMCEFLGLAHCCNLPMLYTFAGYKFRSDLSRLTLKGCTGPASICQQLPFSWRSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 8
US-08-801-228-6
Sequence 6, Application US/0801228
Patent No. 5922541
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
APPLICANT: Wood, William J.
TITLE OF INVENTION: PFAA RECEPTOR NUCLEIC ACID
NUMBER OF SEQUENCES: 6
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801.228
FILING DATE: 19-Feb-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-801-228-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPITLMDLENLEDLFWELDRDNNDNTSLVENVHCPATEGPLMASFKAVFPVAYSL 60
Db 1 MNYPITLMDLENLEDLFWELDRDNNDNTSLVENVHCPATEGPLMASFKAVFPVAYSL 60
Qy 61 IFLGVIGVNVLYVILERHRQRTRSSSTEFLFLAVADLLVFLPAVAFEGSGVWLTGTF 120
Db 61 IFLGVIGVNVLYVILERHRQRTRSSSTEFLFLAVADLLVFLPAVAFEGSGVWLTGTF 120
Qy 121 LCKTVIAHKVNFCSSILLACTAVDRYLAIYHVAYRHRRLSTHTCGCTIWGFLI 180
Db 121 LCKTVIAHKVNFCSSILLACTAVDRYLAIYHVAYRHRRLSTHTCGCTIWGFLI 180
Qy 181 ALPEILPAKVSOGHNSLPRCTPSQENQAEATHAWTSFLYVAGFLPMLVMGCVG 240
Db 181 ALPEILPAKVSOGHNSLPRCTPSQENQAEATHAWTSFLYVAGFLPMLVMGCVG 240
Qy 241 VVHLRLQRQRQRQKAVRVALVTSIFFLCMSPHYIVFLDTLARAKVDNTCKLNGSL 300

Query Match 100.0%; Score 1953; DB 3; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8; 7e-176;
 Matches 372; Conservative 0; Mismatches 0; Gaps 0;

Qy	121 LCKTVIALHKVNFYCSLLACIADYRLIAVHAYHRRLSIHTHTCGTTLVGPILL 180	Db	121 LCKTVIALHKVNFYCSLLACIADYRLIAVHAYHRRLSIHTHTCGTTLVGPILL 180
Qy	181 ALPILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSRFLYHAGFLLPMLYNGWCYVG 240	Db	181 ALPILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSLFLYHAGFLLPMLYNGWCYVG 240
Qy	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300	Db	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300
Qy	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360	Db	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360
Qy	361 SESENATSLTTF 372	Db	361 SESENATSLTTF 372
RESULT 9 US-09-104-296-6			
Sequence 6, Application US/09104296			
Patent No. 6087475			
GENERAL INFORMATION:			
APPLICANT: Lee, James			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: PF4A Receptors			
NUMBER OF SEQUENCES: 6			
CORRESPONDENCE ADDRESS:			
STREET: 1 DNA Way			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94000			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Winpatin (Genentech)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/104,296			
FILING DATE: 24-June-1998			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/701265			
FILING DATE: 22-AUG-1996			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/664228			
FILING DATE: 06-JUN-1996			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/076093			
FILING DATE: 11-JUN-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 07/810782			
FILING DATE: 19-DEC-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: Love, Richard B.			
REGISTRATION NUMBER: 34,659			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 415/225-5530			
TELEX: 415/952-9881			
INFORMATION FOR SEQ ID NO: 6:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 372 amino acids			
TYPE: Amino Acid			
TOPOLOGY: Linear			
US-09-104-296-6			

Query Match 100.0%; Score 1953; DB 3; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8; 7e-176;
 Matches 372; Conservative 0; Mismatches 0; Gaps 0;

Qy	1 MNYPPLTLEMIDLENEDLFWELDNLNDNTS1LYENHLCPATGPLMASPKAVFVPAYSL 60	Db	1 MNYPPLTLEMIDLENEDLFWELDNLNDNTS1LYENHLCPATGPLMASPKAVFVPAYSL 60
Qy	61 IFLLGVIGNVLVILVERHROTRSTTEFLFLAVADLFLVFLPFAVEGSGWVLGTF 120	Db	61 IFLLGVIGNVLVILVERHROTRSTTEFLFLAVADLFLVFLPFAVEGSGWVLGTF 120
Qy	61 IFLLGVIGNVLVILVERHROTRSTTEFLFLAVADLFLVFLPFAVEGSGWVLGTF 120	Db	61 IFLLGVIGNVLVILVERHROTRSTTEFLFLAVADLFLVFLPFAVEGSGWVLGTF 120
Qy	121 LCKTVIALHKVNFYCSLLACTAVDYLAIATHAYHRRLSIIHTCGTTLVGFLL 180	Db	121 LCKTVIALHKVNFYCSLLACTAVDYLAIATHAYHRRLSIIHTCGTTLVGFLL 180
Qy	121 LCKTVIALHKVNFYCSLLACTAVDYLAIATHAYHRRLSIIHTCGTTLVGFLL 180	Db	121 LCKTVIALHKVNFYCSLLACTAVDYLAIATHAYHRRLSIIHTCGTTLVGFLL 180
Qy	181 ALPEILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSRFLYHAGFLLPMLYNGWCYVG 240	Db	181 ALPEILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSRFLYHAGFLLPMLYNGWCYVG 240
Qy	181 ALPEILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSRFLYHAGFLLPMLYNGWCYVG 240	Db	181 ALPEILFAKVSQGHNNSSLRCPFQSQENAEATHAWFTSRFLYHAGFLLPMLYNGWCYVG 240
Qy	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300	Db	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300
Qy	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300	Db	241 VVHLRQAQRPQRQAKVRAVALLYTSSIFLCWSPHYIVFLDTLARIKAVDNTCKLNGSL 300
Qy	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360	Db	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360
Qy	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360	Db	301 PVAITMCCEFLGLAHCCNLPMLYTFAGVKFRPSDLRLLTKGCTGPASLQLCQLFPSSWRSSL 360
Qy	361 SESENATSLTTF 372	Db	361 SESENATSLTTF 372
RESULT 10 US-08-382-493-8			
; Sequence 8, Application US/08982493			
; Parent No. 6110695			
; GENERAL INFORMATION:			
; APPLICANT: Gunn, Michael D			
; APPLICANT: Williams, Lewis T			
; APPLICANT: Cyber, Jason G			
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /			
; TITLE OF INVENTION: Receptor Interactions			
; NUMBER OF SEQUENCES: 6			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP			
; STREET: 75 DENISE DRIVE			
; CITY: HILLSBOROUGH			
; STATE: CALIFORNIA			
; COUNTRY: USA			
; ZIP: 94010			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patin (Genentech)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/104,296			
; FILING DATE: 24-June-1998			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/701265			
; FILING DATE: 22-AUG-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/664228			
; FILING DATE: 06-JUN-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/076093			
; FILING DATE: 11-JUN-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 07/810782			
; FILING DATE: 19-DEC-1991			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Love, Richard B.			
; REGISTRATION NUMBER: 34,659			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 415/225-5530			
; TELEX: 415/952-9881			
; INFORMATION FOR SEQ ID NO: 6:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 372 amino acids			
; TYPE: Amino Acid			
; TOPOLOGY: Linear			
; US-09-104-296-6			

MOLECULE_TYPE: protein
 US-08-982-493-8

Query Match 100.0%; Score 1953; DB 3; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8_7e-176;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
 Db 1 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 60

Qy 61 IFLGVIGNVLVILERHRQTRSSTETLFHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 60
 Db 61 IFLGVIGNVLVILERHRQTRSSTETLFHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 60

Qy 121 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 180
 Db 121 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 180

Qy 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAEATHAWFTSRFLYHAGFLIPMLYNGWCYVG 240
 Db 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAEATHAWFTSRFLYHAGFLIPMLYNGWCYVG 240

Qy 241 VVHLRQAQRPRQAKRVAIRLVTISFFLCPMSPYHIVFLDTLARLKAVDNTCKLNSL 300
 Db 241 VVHLRQAQRPRQAKRVAIRLVTISFFLCPMSPYHIVFLDTLARLKAVDNTCKLNSL 300

Qy 301 PVAITMCFLGLAHCLNPMLYTFAGVKFRSDLSRLLTKGCTGPASLQLFPWRSSL 360
 Db 301 PVAITMCFLGLAHCLNPMLYTFAGVKFRSDLSRLLTKGCTGPASLQLFPWRSSL 360

Db 301 PVAITMCFLGLAHCLNPMLYTFAGVKFRSDLSRLLTKGCTGPASLQLFPWRSSL 360

RESULT 12
 US-09-949-016-10255

Sequence 10255; Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 TITLE OF INVENTION: WITH HUMAN DISEASE,
 FILE REFERENCE: CL0001307
 CURRENT APPLICATION NUMBER: US/09/949.016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SEQ ID NO 10255
 LENGTH: 378
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-10255

Query Match 100.0%; Score 1953; DB 4; Length 378;
 Best Local Similarity 100.0%; Pred. No. 8_9e-176;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
 Db 7 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 66

Qy 61 IFLGVIGNVLVILERHRQTRSSTETFLHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 120
 Db 67 IFLGVIGNVLVILERHRQTRSSTETFLHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 126

Qy 121 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 180
 Db 127 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 186

RESULT 11
 US-09-170-496D-66
 Sequence 66; Application US/09170496D
 Patent No. 655539

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Liaw, Chen W.
 TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Receptors
 FILE REFERENCE: AREN-0040
 CURRENT APPLICATION NUMBER: US/09/170,496D
 CURRENT FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 66
 LENGTH: 372
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-170-496D-66

Query Match 100.0%; Score 1953; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 8_7e-176;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 60
 Db 1 MNYPPLTMDLENEDLFWEILDRLNDYNTSLVENHLCPATGPLMASFKAVFVPAVSL 60

Qy 61 IFLGVIGNVLVILERHRQTRSSTETLFHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 120
 Db 61 IFLGVIGNVLVILERHRQTRSSTETLFHLAVADLLVFLCPATEGPMASFKAVFVPAVSL 120

Qy 121 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 180
 Db 121 LCKTVIALHKVNFCSSILLACIAYDRYLAIIVHAVAHRRLSIIHTCGTIWLGFL 180

Qy 301 PVAITMCFLGLAHCLNPMLYTFAGVKFRSDLSRLLTKGCTGPASLQLFPWRSSL 360
 Db 307 PVAITMCFLGLAHCLNPMLYTFAGVKFRSDLSRLLTKGCTGPASLQLFPWRSSL 366

Qy 361 SESENATSLTF 372
 Db 367 SESENATSLTF 378

RESULT 13
 US-09-170-4 96D-200
 Sequence 200, Application US/09170496D
 Patent No. 6555339
 GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 ATTORNEY: Chalmers, Derek T.
 TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Receptors
 FILE REFERENCE: AREN-0040
 CURRENT APPLICATION NUMBER: US/09/170, 496D
 CURRENT FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 200
 LENGTH: 372
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-170-4 96D-200

Query Match 99.7%; Score 1947; DB 4; Length 372;
 Best Local Similarity 99.7%; Pred. No. 3-2e-175; Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

	Query	Match	Score	DB	Length
Qy	1 MNYPITLEMIDLELFWEIDLRLNYNDTSLENHLCPATEGPMASFKAVFVPAVL	1 MNYPITLEMIDLELFWEIDLRLNYNDTSLENHLCPATEGPMASFKAVFVPAVL	83.7%	3	374;
Db	1 MNYPITLEMIDLELFWEIDLRLNYNDTSLENHLCPATEGPMASFKAVFVPAVL	1 MNYPITLEMIDLELFWEIDLRLNYNDTSLENHLCPATEGPMASFKAVFVPAVL	82.9%	3	374;
Qy	61 IFLISGVIGNLVVLERHQTRSSTETFLHAYADLILVFLPFAVAEGSGVWLGTF	61 IFLISGVIGNLVVLERHQTRSSTETFLHAYADLILVFLPFAVAEGSGVWLGTF	83.7%	3	374;
Db	61 IFLISGVIGNLVVLERHQTRSSTETFLHAYADLILVFLPFAVAEGSGVWLGTF	61 IFLISGVIGNLVVLERHQTRSSTETFLHAYADLILVFLPFAVAEGSGVWLGTF	82.9%	3	374;
Qy	121 LCKTVIALHKVNPFYCSLLACIADVRLAIVAHAYHRRLSIIHFCGTIWLGFL	121 LCKTVIALHKVNPFYCSLLACIADVRLAIVAHAYHRRLSIIHFCGTIWLGFL	83.7%	3	374;
Db	121 LCKTVIALHKVNPFYCSLLACIADVRLAIVAHAYHRRLSIIHFCGTIWLGFL	121 LCKTVIALHKVNPFYCSLLACIADVRLAIVAHAYHRRLSIIHFCGTIWLGFL	82.9%	3	374;
Qy	181 ALPEILFAKYSQGHINNSPRCTFQENQARTHAWFTSRPLYHYAGFLLPMLYNGWCYVG	181 ALPEILFAKYSQGHINNSPRCTFQENQARTHAWFTSRPLYHYAGFLLPMLYNGWCYVG	83.7%	3	374;
Db	181 ALPEILFAKYSQGHINNSPRCTFQENQARTHAWFTSRPLYHYAGFLLPMLYNGWCYVG	181 ALPEILFAKYSQGHINNSPRCTFQENQARTHAWFTSRPLYHYAGFLLPMLYNGWCYVG	82.9%	3	374;
Qy	241 VVHRLRQAQRQPKQAKVARYVAILTISIFFLCWSPYHIVFLDTLARLKAVDNTCKLNSSL	241 VVHRLRQAQRQPKQAKVARYVAILTISIFFLCWSPYHIVFLDTLARLKAVDNTCKLNSSL	83.7%	3	374;
Db	241 VVHRLRQAQRQPKQAKVARYVAILTISIFFLCWSPYHIVFLDTLARLKAVDNTCKLNSSL	241 VVHRLRQAQRQPKQAKVARYVAILTISIFFLCWSPYHIVFLDTLARLKAVDNTCKLNSSL	82.9%	3	374;
Qy	301 PVAITMCEFLGIAHCLNPMLYTFAGVKFRSDSLRLLTGCTGPASLCOLPPSWRSSL	301 PVAITMCEFLGIAHCLNPMLYTFAGVKFRSDSLRLLTGCTGPASLCOLPPSWRSSL	83.7%	3	374;
Db	301 PVAITMCEFLGIAHCLNPMLYTFAGVKFRSDSLRLLTGCTGPASLCOLPPSWRSSL	301 PVAITMCEFLGIAHCLNPMLYTFAGVKFRSDSLRLLTGCTGPASLCOLPPSWRSSL	82.9%	3	374;
Qy	361 SESENATSLTF 372	361 SESENATSLTF 372	83.7%	3	374;
Db	361 SESENATSLTF 372	361 SESENATSLTF 372	82.9%	3	374;

RESULT 14
 US-08-982-4 93-6
 Sequence 6, Application US/08982493
 Patent No. 6110695
 GENERAL INFORMATION:
 APPLICANT: Gunn, Michael D
 APPLICANT: Cyster, Jason G
 APPLICANT: Williams, Lewis T
 TITLE OF INVENTION: Modulating B Lymphocyte Chemokine / Receptor Interactions
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA

RESULT 15
 US-08-719-838-2
 Sequence 2, Application US/08709838
 Patent No. 6140064
 GENERAL INFORMATION:
 APPLICANT: Loetscher, Marcel
 APPLICANT: Moser, Bernhard
 TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Mililitia Drive
 CITY: Lexington
 STATE: MA

COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709, 838
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook Esq., David B.
 REGISTRATION NUMBER: 22, 592
 REFERENCE/DOCKET NUMBER: TKI96-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 368 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-709-838-2

Query Match Score 32.5%; Score 635; DB 3; Length 368;
 Best Local Similarity 40.8%; Pred. No. 9.8e-52;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
 Qy Db
 11 LENLEDLFWELDRDNYNTDSILENHLCPATTEGPLMASFKAYEVPAVSLIFLGVIGVQV 70
 20 LENFESSY---DYGENSED--SCCTSPPCQ---DFSLNFDRAFLPALVSLFLGLGNG 72
 Qy Db
 71 LVLVILERHRQRSSSTPELEHLAVADLLVFLPFAVAYEGSGWNLGTFLCKTVIALHK 130
 73 AVAVVLLSRTALSSTDPELHLAVADTLLVLTPLWAAVDAVQWVRSGLCKVAGALFN 132
 Qy Db
 131 VNFYCSSLLACIAVDRLLAVSHAVHVRHRLSIIHTCGTITWLGVGLLALPBILFAKV 190
 133 INFYAGALLACISFDRLVNLIVBARTOLMTRGPAPVITLCLAVWGLCILPAPDFIEL-- 190
 Qy Db
 191 SOGHHNNSL--PRCTFSQENOASHTWNTSRFLYHAGFLPMVMECYVGVRHLRQA 248
 191 -SAHHDERLNATHQCINPPQVGRT---ALRVQLVAGFLLPVLMACYAHILAVI-LV 244
 Db Qy
 249 QRRPQRQKAVRVAIYLTSFELQWSPYIIVIFLDTLARLKAVDNTCKLNGSLPVATIMCE 308
 245 SRGQRRLRAMRLVVVVVAFALCWTPHLLVLDILMGLAARNCGRESRDVAKSVTS 304
 Qy Db
 309 FGGLAHCLNPMETFAGVKFRSDLSRLTUGCTGPAVLQLEPSVQR-SVLESENAT 367
 305 GLGYMHCCINPLLYAFVGVYKFRERMMLLRLGCPNQGPSSSRDSSWWSE1SEAS 364

Search completed: August 29, 2005, 23:58:34
 Job time : 44 secs

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES
1	1953	100.0	372	9 US-09-104-063-6	Sequence 6, Appli	
2	1953	100.0	372	14 US-10-251-385-66	Sequence 66, Appli	
3	1953	100.0	372	14 US-10-252-567A-60	Sequence 60, Appli	
4	1953	100.0	372	14 US-10-239-123-80	Sequence 80, Appli	
5	1953	100.0	372	15 US-10-166-689-6	Sequence 6, Appli	
6	1953	100.0	378	15 US-10-276-774-2243	Sequence 2243, Ap	
7	1947	99.7	372	14 US-10-251-385-200	Sequence 200, App	
8	1938.5	99.3	371	20 US-11-021-951-154	Sequence 84, Appli	
9	635	32.5	368	14 US-10-251-385-20	Sequence 20, Appli	
10	635	32.5	368	14 US-10-252-567A-74	Sequence 74, Appli	
11	635	32.5	368	14 US-10-345-680-59	Sequence 59, Appli	

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2C2
 TELEPHONE: 415/225-5520
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-104-063-6

Query Match 100.0%; Score 1953; DB 14; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.6e-165;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60
 Db 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60

Qy 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120
 Db 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120

Qy 61 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180
 Db 121 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180

Qy 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240
 Db 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240

Qy 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60
 Db 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60

Qy 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120
 Db 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120

Qy 121 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180
 Db 121 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180

Qy 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240
 Db 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240

Qy 241 VVHLRQAQRPRQKAVRVALLTSPFLCWSPHYIVFLDPLARLKAVDNTCKLNSL 300
 Db 241 VVHLRQAQRPRQKAVRVALLTSPFLCWSPHYIVFLDPLARLKAVDNTCKLNSL 300

Qy 301 PVATMCEFGLAHCCLNPMLYTFAGVKERSDSLRLTTLKGCTGPASLQLFPSSWRSSL 360
 Db 301 PVATMCEFGLAHCCLNPMLYTFAGVKERSDSLRLTTLKGCTGPASLQLFPSSWRSSL 360

Qy 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240
 Db 181 ALPEILPAKVSQGHNSLPRCTFSQENQAEATHAWFTSRFLYHAGFLLPMLVGMWCYVG 240

Qy 241 VVHLRQAQRPRQKAVRVALLTSPFLCWSPHYIVFLDPLARLKAVDNTCKLNSL 300
 Db 241 VVHLRQAQRPRQKAVRVALLTSPFLCWSPHYIVFLDPLARLKAVDNTCKLNSL 300

Qy 301 PVATMCEFGLAHCCLNPMLYTFAGVKERSDSLRLTTLKGCTGPASLQLFPSSWRSSL 360
 Db 301 PVATMCEFGLAHCCLNPMLYTFAGVKERSDSLRLTTLKGCTGPASLQLFPSSWRSSL 360

Qy 361 SESENATSLTF 372
 Db 361 SESENATSLTF 372

RESULT 3
 US-10-225-567A-60
 Sequence 60, Application US/10225567A
 Publication No. US20030113798A1
 GENERAL INFORMATION:
 APPLICANT: LifeSpan Biosciences
 Brown, Joseph P.
 BURMER, Christine C.
 ROUSH, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTC
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 60
 LENGTH: 372
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-225-567A-60

Query Match 100.0%; Score 1953; DB 14; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.6e-165;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60
 Db 1 MNYPPLTEMDLENLEDLFWELDRLDNYNDTSLVEHNLCPATGSPLMASFKAFFVFPVAYSL 60

Qy 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120
 Db 61 IFPLGVIGNVLVILERHRQTRSSTETFLFLAVADLLVPTLPFAVAEGSGVWLGTF 120

Qy 61 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180
 Db 121 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180

Qy 121 LCKTVIALHKVNKFYCSILLACIADVRLAIVHAYRHRRLSIIHTCGTIWLGFL 180

Publication No. US20040053245A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc., Tom et al.
 TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
 FILE REFERENCE: 21272-030
 CURRENT APPLICATION NUMBER: US/10/276,774
 CURRENT FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: 09/560,875
 PRIORITY FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 09/496,914
 NUMBER OF SEQ ID NOS: 2700
 SOFTWARE: Custom
 SEQ ID NO: 2243
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-276-774-2243

Query Match 100.0%; Score 1953; DB 15; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-15;
 Matches 372; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MNYPITLMDLENLDLFWELDRDNYNDTSILVENVHLCPATGPIMASFKAVFVPAVSL 60
 Db 7 MNYPITLMDLENLDLFWELDRDNYNDTSILVENVHLCPATGPIMASFKAVFVPAVSL 66

Qy 61 IFLGVGNVLVILVERHRQTSSTEFLWELDRDNYNDTSILVENVHLCPATGPIMASFKAVFVPAVSL 120
 Db 67 IFLGVGNVLVILVERHRQTSSTEFLWELDRDNYNDTSILVENVHLCPATGPIMASFKAVFVPAVSL 126

Qy 121 LCKTVIALEHKVNFCSSLLACIADYRLIAVHAYRHRLLSIHTCGTIWLGFL 180
 Db 127 LCKTVIALEHKVNFCSSLLACIADYRLIAVHAYRHRLLSIHTCGTIWLGFL 186

Qy 181 ALPELFKAVSOGHHNSLPRCTFSQENQAEHWATSRFLYVAGFLPMLVMGRCVG 240
 Db 187 ALPELFKAVSOGHHNSLPRCTFSQENQAEHWATSRFLYVAGFLPMLVMGRCVG 246

RESULT 8
 US-11-021-951-154
 Sequence 154, Application US/11/021,951
 Publication No. US20050175581A1
 GENERAL INFORMATION:
 APPLICANT: HAUPPS, Ulrich
 APPARTANT: KOLTERMANN, Andre
 APPARTANT: SCHEIDIG, Andreas
 APPARTANT: VETTERER, Christian
 APPARTANT: Kettling, Ulrich
 APPARTANT: COCO, Wayne Michael
 TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
 Title of Invention: And Diagnostic Use Thereof
 FILE REFERENCE: 04156.0002US
 CURRENT FILING DATE: 2004-12-22
 PRIOR APPLICATION NUMBER: 10/872,198
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 60/543,518
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/524,960
 PRIOR FILING DATE: 2003-11-25
 PRIOR APPLICATION NUMBER: EP 04003058
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: EP 03025871
 PRIOR FILING DATE: 2003-11-11
 PRIOR APPLICATION NUMBER: EP 03025851
 PRIOR FILING DATE: 2003-11-10
 PRIOR APPLICATION NUMBER: EP 03013819
 PRIOR FILING DATE: 2003-06-18
 NUMBER OF SEQ ID NOS: 191
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 154
 LENGTH: 371
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 7
 US-10-251-385-200
 Sequence 200, Application US/10251385
 Publication No. US20030105292A1
 GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Liaw, Chen W.
 TITLE OF INVENTION: Activated Human G Protein-Coupled Receptors
 TITLE OF INVENTION: Receptors
 FILE REFERENCE: ARIEN-0040
 CURRENT APPLICATION NUMBER: US/10/251,385
 CURRENT FILING DATE: 2002-09-20
 PRIOR APPLICATION NUMBER: EP 03013819
 PRIOR FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 200
 LENGTH: 372

us-11-021-951-154

Query Match 99.3%; Score 1938.5; DB 20; Length 371;
Best Local Similarity 99.7%; Pred. No. 3.1e-164;
Matches 371; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MNYPITLLEMIDLENLEDWFELDRDNYNDTSVLVENHLCPATEGPLMASPKAVFVPAVSL 60
Db 1 MNYPITLLEMIDLENLEDWFELDRDNYNDTSVLVENHLCPATEGPLMASPKAVFVPAVSL 60

Qy 61 IFLLGTVGIVNLVLTLEHRROTSSTETFFLFLHAYADLLIILFVLPFAVAEGSVGMWLGTF 120
Db 61 IFLLGTVGIVNLVLTLEHRROTSSTETFFLFLHAYADLLIILFVLPFAVAEGSVGMWLGTF 120

Qy 121 LCKTVTAHKCONFYCSSILLACIATDVRLAIIHVAYHRRRLSIHICGTWLVGFLL 180
Db 121 LCKTVTAHKCONFYCSSILLACIATDVRLAIIHVAYHRRRLSIHICGTWLVGFLL 180

Qy 181 ALPELFKAVSQGHINNSLRPCTFSQENQAEATHAWFTSREPLHYAGFLLPMLYNGWCYVG 240
Db 181 ALPELFKAVSQGHINNSLRPCTFSQENQAEATHAWFTSREPLHYAGFLLPMLYNGWCYVG 240

Qy 241 VVHLRQAORRPOROKAVRVALLYTISIFFLCSWPYHIVTFLDTLARLKAVDNTCKLNGL 300
Db 241 -VVHLRQAORRPOROKAVRVALLYTISIFFLCSWPYHIVTFLDTLARLKAVDNTCKLNGL 299

Qy 301 PVALTMCEFLGLANCPMLYTAGVFKERSDSLRLTFLGCTGPASLQLPWSWRSSL 360
Db 300 PVALTMCEFLGLANCPMLYTAGVFKERSDSLRLTFLGCTGPASLQLPWSWRSSL 359

Qy 361 SESENATSLTTF 372
Db 360 SESENATSLTTF 371

RESULT 9
US-10-251-385-20
; Sequence 20, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Benan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Law, Chen W.
; TITLE OF INVENTION: US 20030105292A1 - Endogenous, Constitutively Activated Human G Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: ARBN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 20
; LENGTH: 368

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Qy 11 LENLEDLFWEDLRLDNYNTDSLIVENHLCPATEGPLMASPKAVFVPAVSL 32.5%; Score 635; DB 14; Length 368;
Db 11 LENLEDLFWEDLRLDNYNTDSLIVENHLCPATEGPLMASPKAVFVPAVSL 32.5%; Score 635; DB 14; Length 368;
; Sequence 74, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Gleena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-44
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 74
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 74
; LENGTH: 368

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Qy 12 20 LENFSSYY--DYGENSESD-SCTSPPCQ--DEFSNEDFLPAPYSLFLGLJLQNG 72
Db 12 20 LENFSSYY--DYGENSESD-SCTSPPCQ--DEFSNEDFLPAPYSLFLGLJLQNG 72

Qy 71 LYVLVILERHRQTSSSETFLFLHAYADLLVFLPFAVAEGSVGVNLGFLKTIVLHK 130
Db 73 AVAVLISRRTALSSDTFLHAYADLLVFLPWAQVYFGSGLCKVAGALFN 132

Qy 131 VNFCYSSLLACIATDVRLAIIHVAYHRRRLSIHITCCTIWLYGFLALPEILFAKV 190
Db 133 INFYAGALLACIATDVRLAIIHVAYHRRRLSIHITCCTIWLYGFLALPEILFAKV 190

Qy 191 SGHHNNSL--PRCTFSQENQAEATHAWFTSREPLHYAGFLLPMLYNGWCYGVVHLRQA 248
Db 191 -SAHDERLNRATHCQNFQVGRTE--ALRVLQVAGFLLPMLYNGWCYGVVHLRQA 248

Qy 249 QRRPQRQKAVRVALLYTISIFFLCSWPYHIVTFLDTLARLKAVDNTCKLNGLPVAITMC 308
Db 245 SRGQRRLRAMLVYVYVVAFALCWTYFLVYLVDTLMDLGALARNGRESRVDVAKSVTS 304

Qy 309 FLGLAHCCCLNPMLYTAGVFKERSDSLRLTFLGCTGPASLQLPWSWRRL-SSLSESENAT 367
Db 305 GLGYMHCCCLNPMLYAFGVKFERRMMILLRGCPNQRGQLQROPSSSRRDSSWSETSEAS 364

RESULT 11
US-10-345-680-59
; Sequence 59, Application US/10345680
; Publication No. US2003014894A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

Qy 71 LYVLVILERHRQTSSSETFLFLHAYADLLVFLPFAVAEGSVGVNLGFLKTIVLHK 130
Db 73 AVAVLISRRTALSSDTFLHAYADLLVFLPWAQVYFGSGLCKVAGALFN 132
Qy 131 VNFCYSSLLACIATDVRLAIIHVAYHRRRLSIHITCCTIWLYGFLALPEILFAKV 190

APPLICANT: Silos-Santiago, Inmaculada
 APPLICANT: Venkateswarlu, Karichetti
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1335, 559, 34021, 44999, 252278,
 TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 TITLE OF INVENTION: 12301, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 FILE REFERENCE: MP102-012P1RN OMNI
 CURRENT APPLICATION NUMBER: US710/345, 680
 CURRENT FILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US 60/349, 511

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US 60/360, 500

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/365, 041

PRIOR FILING DATE: 2002-03-15

PRIOR APPLICATION NUMBER: US 60/374, 063

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US 60/403, 468

PRIOR FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: US 60/414, 262

PRIOR FILING DATE: 2002-09-27

PRIOR APPLICATION NUMBER: US 60/419, 986

PRIOR FILING DATE: 2002-10-21

PRIOR APPLICATION NUMBER: US 60/423, 809

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 60/429, 797

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 66

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 59

LENGTH: 368

TYPE: PR

ORGANISM: Homo Sapiens

US-10-345-680-59

Query Match Score 635; DB 14; Length 368;

Best Local Similarity 40.8%; Pred. No. 4.2e-48;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

US-10-251-686-2

Query Match Score 635; DB 14; Length 368;

Best Local Similarity 40.8%; Pred. No. 4.2e-48;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Qy 11 LENEDLFWELDRNDNYNTDSLVENHCPATEGPLMASPKAVFPVAYSLIFLGVICNV 70
 Db 20 LENFSSYY --DYGENSED-SCCTSPPCPQ-- -DESLNFDRAFLPALMSLFLGLUNG 72

Qy 71 LVLVILERHRQRTRSSSTTEFLHLAVADLLVFLPFAVAGSGVWLGCTFLCKTVIAHLK 130
 Db 73 AVALVLSRRTALESSTDEFLHLAVADTLVLPLWDAVQWVFESSGLCKVAGALFN 132

Qy 131 VNFYCSSLLIACIAYDRYLAIHVAVAHYHRRLISIHITCGTIVLWVGJLALPEILFKV 190
 Db 133 INFAGALLACISDRLNVIVHTQLYRGPPARVLTCLAVWGLCILFALPDFIFU-- 190

Qy 191 SQGHHNSSL--PRCTFSOENQAETHAWFTSRFLYHAGFLPMLVMGWCYVGVHRLRQA 248
 Db 191 -SAHHDERLNATHCQYNPQVGRT---AIRVLQLQVAGTLPVLMVAMYAHILAVI-LV 244

Db 191 SRGQRRLRAMRLVWVVVAFAICWTPHLYVLDIMLGALARNCGRESRVDAKSVT 304

Qy 249 QRRPQRQKAVALVLTSTFLCNPSHYVFLDTLRLKAVDNTCKLNGSLPVAITMC 308
 Db 245 SRGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367

Qy 309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367
 Db 305 GLGMHMHCCLNPMLIYAFVGKFRERMMMLLRLGPNRQSSRRDSSMSETSEAS 364

Qy 309 FGGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367
 Db 305 GLGMHMHCCLNPMLIYAFVGKFRERMMMLLRLGPNRQSSRRDSSMSETSEAS 364

RESULT 12

US-10-251-686-2

Sequence 2, Application US10251686

Publication No. US20030158392A1

GENERAL INFORMATION:

APPLICANT: Loetscher, Marcel

Moser, Bernhard

Qin, Shixin

Mackay, Charles R.

TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
 CITY: Lexington

STATE: MA
 COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/251, 686

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/829, 839

FILING DATE: 31-Mar-1997

APPLICATION NUMBER: US 08/709, 838

FILING DATE: 10-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brook Esq., David E.

REGISTRATION NUMBER: 22, 592

REFERENCE/DOCKET NUMBER: TK196-01A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 368 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match Score 635; DB 14; Length 368;

Best Local Similarity 40.8%; Pred. No. 4.2e-48;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Qy 11 LENEDLFWELDRNDNYNTDSLVENHCPATEGPLMASPKAVFPVAYSLIFLGVICNV 70
 Db 20 LENFSSYY --DYGENSED-SCCTSPPCPQ-- -DESLNFDRAFLPALMSLFLGLUNG 72

Qy 11 LENEDLFWELDRNDNYNTDSLVENHCPATEGPLMASPKAVFPVAYSLIFLGVICNV 70
 Db 20 LENFSSYY --DYGENSED-SCCTSPPCPQ-- -DESLNFDRAFLPALMSLFLGLUNG 72

Qy 71 LVLVILERHRQRTRSSSTTEFLHLAVADLLVFLPFAVAGSGVWLGCTFLCKTVIAHLK 130
 Db 73 AVALVLSRRTALESSTDEFLHLAVADTLVLPLWDAVQWVFESSGLCKVAGALFN 132

Qy 71 LVLVILERHRQRTRSSSTTEFLHLAVADLLVFLPFAVAGSGVWLGCTFLCKTVIAHLK 130
 Db 73 AVALVLSRRTALESSTDEFLHLAVADTLVLPLWDAVQWVFESSGLCKVAGALFN 132

Qy 131 VNFYCSSLLIACIAYDRYLAIHVAVAHYHRRLISIHITCGTIVLWVGJLALPEILFKV 190
 Db 133 INFAGALLACTSDFLNLVITPLWDAVQWVFESSGLCKVAGALFN 190

Qy 191 SQGHHNSSL--PRCTFSOENQAETHAWFTSRFLYHAGFLPMLVMGWCYVGVHRLRQA 248
 Db 191 -SAHHDERLNATHCQYNPQVGRT---ALRVQLYAGFLPMLVMAYCAHILAVI-LV 244

Db 191 SAHHDERLNATHCQYNPQVGRT---ALRVQLYAGFLPMLVMAYCAHILAVI-LV 244

Db 191 SRGQRRLRAMRLVWVVVAFAICWTPHLYVLDIMLGALARNCGRESRVDAKSVT 304

Qy 249 QRRPQRQKAVALVLTSTFLCNPSHYVFLDTLRLKAVDNTCKLNGSLPVAITMC 308
 Db 245 SRGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367

Qy 309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367
 Db 305 GLGMHMHCCLNPMLIYAFVGKFRERMMMLLRLGPNRQSSRRDSSMSETSEAS 364

Qy 309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKGTGPASLQLCOPPSWR-SSLESEENAT 367
 Db 305 GLGMHMHCCLNPMLIYAFVGKFRERMMMLLRLGPNRQSSRRDSSMSETSEAS 364

RESULT 13

US-10-239-423-78

Sequence 78, Application US10239423

Publication No. US20030186885A1

Publication Date: 2003-03-01

GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HETTLAND, Aleksandra; SPODBERG, Nikolaj;
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; Cell Surface Proteome of Tumor and Inflammation Cells and
; For Treating Tumor Diseases and Inflammatory Diseases,
; Preferably with the Aid of Specific Chemokine
; Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217.us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIORITY NUMBER: DE10016013.1
; PRIORITY FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 78
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
; US-10-239-423-78

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Qy 11 LENLEDLWELDLDNYNTDSVLVENHLCPATGEPMLMASFKAVFVPAVSLIFLGIVGNV 70
Db 20 LENFSSSY--DGYENSD--SCCTSPPCQ--DFSLNFDRAFLPALSLLFLPLGLING 72

Qy 71 LVLVILERHRQTSSTEFLPHLAVADLLVFLLPAVAGSIVGWUJTFLLCTVIAHK 130
Db 73 AVAVALLSRTTALSSTDELLHLAVADTLLVTLPLWADAVQWVFGSLCKVAGLFN 132

RESULT 15
US-10-295-027-752
; Sequence 752, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezsi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Bio Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13

RESULT 14
US-10-411-284-4
; Sequence 4, Application US/10411284
; Publication No. US20030244265A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSAT6B
; CURRENT APPLICATION NUMBER: US/10/411,284
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,725
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/101,518
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: PCT/US96/00499
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 4
; LENGTH: 368

i Remaining Prior Application data removed - See File Wrapper or PAML.
i NUMBER OF SEQ ID NOS: 1386
i SOFTWARE: PatentIn Ver. 2.1
i SEQ ID NO: 752
i LENGTH: 368
i TYPE: PRT
i ORGANISM: Homo sapiens
US-10-293-027-752

Query Match	32.5%	Score 635;	DB 15;	Length:368;
Best Local Similarity	40.8%	Pred. No. 4-28-48;		
Matches	147	Conservative	50;	Mismatches 145; Indels 18; Gaps 8;

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Qy          11 LENLEDFWFELDRDLNNDTSVLVENHLCPATGPIIMASPKAVFVPAVASLIFLGVICNV 70
Db          20 LENFESSY--DYGNEESD-SCCNSPPCPRQ---DEFLNIDRAEFLPALISLLEFLIGLNG 72
Qy          71 LVLVTLERIHRQTRSSTTEFLFHLLAVADLLVFLPFAVEGSYCWGLGTFLCKTVIAHK 130
Db          73 ARAVAVLSSRATLSSSTDFFLHLAVADTFLVTLPLWAVDAAYQWVFESSGLCKVAGALFN 132
Qy          131 VNFYCSSLILACIAYDRYLAIIVHAYAIVHRLLIISHTHRCGTVWLVGFLALPBLFLFKV 190
Db          133 INFYAGALLIACISDRYLNIIVHATQLVLRGGPPARVTICLAWGLCLFLALPDFIF-- 190
Qy          191 SGQHHNNNSI--PRCTFSQENOAETHAWFTSRSFLYHVAGFLPMLVMGCVYGVHRLRQA 248
Db          191 -SAHHDERINATHCOYNFOYGRT---AIRVLOLVAGFLPLIVMAYCAHTIHLAVL-LV 244
Qy          249 QRRPQRQAVRVALIVTSIFFLCKMSPTMIVFELDTLARKAVDNTCKNGSLPEVATMCE 308
Db          245 SRGQRRLRANRLVYVVVVAFAFCMTPTHUVLVDILMDIGALARNCGRSRDVAKSYTS 304
Qy          309 FGLIAHCINPMLYTFAGYKFRSDISRLITKLGETGPASLCQLPSSWR-SSEUSEVAT 367
Db          305 GLGYMHACINPMLYAFGVKFRERMMLLRLGCNPQRQOPSSRRDSSWSETSEAS 364

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Search completed: August 30, 2005, 00:01:24
 Job time : 166 secs